

Sequence Listing

- <110> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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<210> 10
<211> 319
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<213> Homo sapiens
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<223> Signal Peptide
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<221> misc feature
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215 220 225

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230 235 240

Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser
245 250 255

Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His
260 265 270

Ala Leu Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys
275 280 285

Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala
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Leu Gln Asp Phe Leu Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn
305 310 315

Pro Lys Ala Val

<210> 11
<211> 2720
<212> DNA
<213> Homo sapiens

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<210> 12
<211> 699
<212> PRT
<213> Homo sapiens
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<220>
<221> TRANSMEM
<222> 21-40 and 84-105
<223> Transmembrane Domain (type II)
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				20					25					30	
Val	Ala	Thr	Thr	Val	Val	Met	Tyr	Pro	Pro	Pro	Pro	Pro	Pro	Pro	
				35					40					45	
His	Arg	Asp	Phe	Ile	Ser	Val	Thr	Leu	Ser	Phe	Gly	Glu	Ser	Tyr	
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Asp	Asn	Ser	Lys	Ser	Trp	Arg	Arg	Arg	Ser	Cys	Trp	Arg	Lys	Trp	
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Lys	Gln	Leu	Ser	Arg	Leu	Gln	Arg	Asn	Met	Ile	Leu	Phe	Leu	Leu	
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Ala	Phe	Leu	Leu	Phe	Cys	Gly	Leu	Leu	Phe	Tyr	Ile	Asn	Leu	Ala	
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Asp	His	Trp	Lys	Ala 110	Leu	Ala	Phe	Arg	Leu 115	Glu	Glu	Glu	Gln	Lys 120
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Leu	Pro	Ala	Pro	Gln 140	Lys	Ala	Asp	Thr	Asp 145	Pro	Glu	Asn	Leu	Pro 150
Glu	Ile	Ser	Ser	Gln 155	Lys	Thr	Gln	Arg	His 160	Ile	Gln	Arg	Gly	Pro 165
Pro	His	Leu	Gln	Ile 170	Arg	Pro	Pro	Ser	Gln 175	Asp	Leu	Lys	Asp	Gly 180
Thr	Gln	Glu	Glu	Ala 185	Thr	Lys	Arg	Gln	Glu 190	Ala	Pro	Val	Asp	Pro 195
Arg	Pro	Glu	Gly	Asp 200	Pro	Gln	Arg	Thr	Val 205	Ile	Ser	Trp	Arg	Gly 210
Ala	Val	Ile	Glu	Pro 215	Glu	Gln	Gly	Thr	Glu 220	Leu	Pro	Ser	Arg	Arg 225
Ala	Glu	Val	Pro	Thr 230	Lys	Pro	Pro	Leu	Pro 235	Pro	Ala	Arg	Thr	Gln 240
Gly	Thr	Pro	Val	His 245	Leu	Asn	Tyr	Arg	Gln 250	Lys	Gly	Val	Ile	Asp 255
Val	Phe	Leu	His	Ala 260	Trp	Lys	Gly	Tyr	Arg 265	Lys	Phe	Ala	Trp	Gly 270
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Gly	Leu	Gly	Leu	Thr 290	Leu	Ile	Asp	Ala	Leu 295	Asp	Thr	Met	Trp	Ile 300
Leu	Gly	Leu	Arg	Lys 305	Glu	Phe	Glu	Glu	Ala 310	Arg	Lys	Trp	Val	Ser 315
Lys	Lys	Leu	His	Phe 320	Glu	Lys	Asp	Val	Asp 325	Val	Asn	Leu	Phe	Glu 330
Ser	Thr	Ile	Arg	Ile 335	Leu	Gly	Gly	Leu	Leu 340	Ser	Ala	Tyr	His	Leu 345
Ser	Gly	Asp	Ser	Leu 350	Phe	Leu	Arg	Lys	Ala 355	Glu	Asp	Phe	Gly	Asn 360
Arg	Leu	Met	Pro	Ala 365	Phe	Arg	Thr	Pro	Ser 370	Lys	Ile	Pro	Tyr	Ser 375
Asp	Val	Asn	Ile	Gly 380	Thr	Gly	Val	Ala	His 385	Pro	Pro	Arg	Trp	Thr 390
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe

395					400					405						
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Asp	Gly	Leu	Val	440	Pro	Met	Phe	Ile	Asn	Thr	His	Ser	Gly	Leu	Phe	450
Thr	His	Leu	Gly	455	Val	Phe	Thr	Leu	Gly	Ala	Arg	Ala	Asp	Ser	Tyr	465
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Thr	Gln	Leu	Leu	485	Glu	Asp	Tyr	Val	Glu	Ala	Ile	Glu	Gly	Val	Arg	495
Thr	His	Leu	Leu	500	Arg	His	Ser	Glu	Pro	Ser	Lys	Leu	Thr	Phe	Val	510
Gly	Glu	Leu	Ala	515	His	Gly	Arg	Phe	Ser	Ala	Lys	Met	Asp	His	Leu	525
Val	Cys	Phe	Leu	530	Pro	Gly	Thr	Leu	Ala	Leu	Gly	Val	Tyr	His	Gly	540
Leu	Pro	Ala	Ser	545	His	Met	Glu	Leu	Ala	Gln	Glu	Leu	Met	Glu	Thr	555
Cys	Tyr	Gln	Met	560	Asn	Arg	Gln	Met	Glu	Thr	Gly	Leu	Ser	Pro	Glu	570
Ile	Val	His	Phe	575	Asn	Leu	Tyr	Pro	Gln	Pro	Gly	Arg	Arg	Asp	Val	585
Glu	Val	Lys	Pro	590	Ala	Asp	Arg	His	Asn	Leu	Leu	Arg	Pro	Glu	Thr	600
Val	Glu	Ser	Leu	605	Phe	Tyr	Leu	Tyr	Arg	Val	Thr	Gly	Asp	Arg	Lys	615
Tyr	Gln	Asp	Trp	620	Gly	Trp	Glu	Ile	Leu	Gln	Ser	Phe	Ser	Arg	Phe	630
Thr	Arg	Val	Pro	635	Ser	Gly	Gly	Tyr	Ser	Ser	Ile	Asn	Asn	Val	Gln	645
Asp	Pro	Gln	Lys	650	Pro	Glu	Pro	Arg	Asp	Lys	Met	Glu	Ser	Phe	Phe	660
Leu	Gly	Glu	Thr	665	Leu	Lys	Tyr	Leu	Phe	Leu	Leu	Phe	Ser	Asp	Asp	675
Pro	Asn	Leu	Leu	680	Ser	Leu	Asp	Ala	Tyr	Val	Phe	Asn	Thr	Glu	Ala	690

His Pro Leu Pro Ile Trp Thr Pro Ala
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<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
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ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgctgg 200
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aaaaaaaaaa aaaaaaaaaa aaaa 1524

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<210> 17
<211> 327
<212> PRT
<213> Homo sapiens
<220>
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<221> sig_peptide
<222> 1-42
<223> Signal peptide.

<220>
<221> misc_feature
<222> 19-25, 65-71, 247-253, 285-291, 303-310
<223> N-myristoylation site.

<220>
<221> misc_feature
<222> 27-31
<223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
<221> TRANSMEM
<222> 29-49
<223> Transmembrane domain (type II).

<220>
<221> misc_feature
<222> 154-158
<223> N-glycosylation site.

<220>
<221> misc_feature
<222> 226-233
<223> Tyrosine kinase phosphorylation site.

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35 40 45
Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
50 55 60
Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
65 70 75
Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
80 85 90
Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
95 100 105
Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
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Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
125 130 135
His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

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Leu Leu Pro Leu Asn Glu Glu Leu Asp	Tyr Gly Phe Pro Glu Ala	
170	175	180
Gly Pro Phe His Val Ala Ser Pro Glu	Leu His Pro Leu Tyr His	
185	190	195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu	Leu Leu Ser Lys Gln His	
200	205	210
Tyr Arg Leu Cys Asn Gly Met Ser Asn	Arg Phe Trp Gly Trp Gly	
215	220	225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg	Ile Lys Gly Ala Gly Leu	
230	235	240
Gln Leu Phe Arg Pro Ser Gly Ile Thr	Thr Gly Tyr Lys Thr Phe	
245	250	255
Arg His Leu His Asp Pro Ala Trp Arg	Lys Arg Asp Gln Lys Arg	
260	265	270
Ile Ala Ala Gln Lys Gln Glu Gln Phe	Lys Val Asp Arg Glu Gly	
275	280	285
Gly Leu Asn Thr Val Lys Tyr His Val	Ala Ser Arg Thr Ala Leu	
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Ser Val Gly Gly Ala Pro Cys Thr Val	Leu Asn Ile Met Leu Asp	
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Cys Asp Lys Thr Ala Thr Pro Trp Cys	Thr Phe Ser	
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<210> 18
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 18
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<210> 19
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-24
<223> Synthetic construct

<400> 19
gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 20
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
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gactggtcgg tgcccagaaa gtctcttctg ccaactgacgc ccccatcagg 150
gattgggcct tctttccccc ttcctttctg tgtctcctgc ctcatcggcc 200
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ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350
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taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

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Ser	Cys	Leu	Glu	Trp	Gly	Leu	Val	Gly	Ala	Gln	Lys	Val	Ser
			20					25					30
Ala	Thr	Asp	Ala	Pro	Ile	Arg	Asp	Trp	Ala	Phe	Phe	Pro	Pro
			35					40					45
Phe	Leu	Cys	Leu	Leu	Pro	His	Arg	Pro	Ala	Met	Thr	Cys	Ser
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Ala	Gln	Pro	Arg	Gly	Glu	Gly	Glu	Lys	Val	Gly	Asp	Gly	
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<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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<210> 24
<211> 616
<212> PRT
<213> Homo sapiens
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<221> sig_peptide
<222> 1-33
<223> Signal peptide.
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<220>
<221> TRANSMEM
<222> 13-40
<223> Transmembrane domain (type II).
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Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His
          35          40          45

Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
          50          55          60

Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
          65          70          75

Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
          80          85          90

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Asn Lys Ile Ser Glu Leu Lys Asn Gly Ser Phe Ser Gly Leu Ser	95	100	105
Leu Leu Glu Arg Leu Asp Leu Arg Asn Asn Leu Ile Ser Ser Ile	110	115	120
Asp Pro Gly Ala Phe Trp Gly Leu Ser Ser Leu Lys Arg Leu Asp	125	130	135
Leu Thr Asn Asn Arg Ile Gly Cys Leu Asn Ala Asp Ile Phe Arg	140	145	150
Gly Leu Thr Asn Leu Val Arg Leu Asn Leu Ser Gly Asn Leu Phe	155	160	165
Ser Ser Leu Ser Gln Gly Thr Phe Asp Tyr Leu Ala Ser Leu Arg	170	175	180
Ser Leu Glu Phe Gln Thr Glu Tyr Leu Leu Cys Asp Cys Asn Ile	185	190	195
Leu Trp Met His Arg Trp Val Lys Glu Lys Asn Ile Thr Val Arg	200	205	210
Asp Thr Arg Cys Val Tyr Pro Lys Ser Leu Gln Ala Gln Pro Val	215	220	225
Thr Gly Val Lys Gln Glu Leu Leu Thr Cys Asp Pro Pro Leu Glu	230	235	240
Leu Pro Ser Phe Tyr Met Thr Pro Ser His Arg Gln Val Val Phe	245	250	255
Glu Gly Asp Ser Leu Pro Phe Gln Cys Met Ala Ser Tyr Ile Asp	260	265	270
Gln Asp Met Gln Val Leu Trp Tyr Gln Asp Gly Arg Ile Val Glu	275	280	285
Thr Asp Glu Ser Gln Gly Ile Phe Val Glu Lys Asn Met Ile His	290	295	300
Asn Cys Ser Leu Ile Ala Ser Ala Leu Thr Ile Ser Asn Ile Gln	305	310	315
Ala Gly Ser Thr Gly Asn Trp Gly Cys His Val Gln Thr Lys Arg	320	325	330
Gly Asn Asn Thr Arg Thr Val Asp Ile Val Val Leu Glu Ser Ser	335	340	345
Ala Gln Tyr Cys Pro Pro Glu Arg Val Val Asn Asn Lys Gly Asp	350	355	360
Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr Ala Tyr Leu Gln	365	370	375
Cys Thr Arg Asn Thr His Gly Ser Gly Ile Tyr Pro Gly Asn Pro			

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<210> 25
<211> 24
<212> DNA
<213> Artificial
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33

<223> Synthetic construct

<400> 25
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<210> 26
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 26
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<210> 27
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 27
gtaaaggaga agaacatcac ggtacgggat accaggtgtg tttatcctaa 50

<210> 28
<211> 683
<212> DNA
<213> Homo sapiens

<400> 28
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gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcggg 150
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atgacttgaa tgtgaaatat ctgttgga gacaacacga gtttgtgtgt 300
gtgtgttgat ggagagtagc ttagtagtat cttcatcttt ttttttggtc 350
actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400
ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450
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tgtccagtgc ttagggttgt tactgagaag cactgccgag cttgtgagaa 550

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 gtggagggag agacgctcct gatcgctgaa tcc 683

<210> 29
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> 1-21
 <223> Signal peptide.

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 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
 35 40 45
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
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 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
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 Lys Gly Ser Gln Lys Ser
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<210> 30
 <211> 2128
 <212> DNA
 <213> Homo sapiens

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 tccgtggatt cctctgctaa gaccgctgcc atgccagtga cggtaaccgc 150
 caccaccatc acaaccacca cgacgtcatc ttcgggcctg ggggtcccca 200
 tgatcgtggg gtcccctcgg gccctgacac agcccctggg tctccttcgc 250
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accttcttct	cctgcatcgc	gtgtgtggct	tacgccaccg	aagtggcctg	600
gacccggggc	cggccccggc	agatcactgg	ctatatggcc	accgtacccg	650
ggctgctgaa	ggtgctggag	accttcgttg	cctgcatcat	cttcgcgttc	700
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 <211> 322
 <212> PRT
 <213> Homo sapiens

<400> 31
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 Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val
 35 40 45
 Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
 50 55 60
 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
 65 70 75
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
 80 85 90
 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
 95 100 105
 Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr
 110 115 120
 Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
 125 130 135
 His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala
 140 145 150
 Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile
 155 160 165
 Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu
 170 175 180
 Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn
 185 190 195
 Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr
 200 205 210

Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu
 215 220 225

Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu
 230 235 240

Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu
 245 250 255

Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln
 260 265 270

Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr
 275 280 285

Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr
 290 295 300

Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala
 305 310 315

His Leu Val Phe Val Lys Val
 320

<210> 32
 <211> 3680
 <212> DNA
 <213> Homo sapiens

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<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

Met Phe Leu Ala Thr Leu Ser Phe Leu Leu Pro Phe Ala His Pro
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Phe Gly Thr Val Ser Cys Glu Tyr Met Leu Gly Ser Pro Leu Ser
20 25 30

Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val
35 40 45

His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu
50 55 60

Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu
65 70 75

Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro
80 85 90

Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys
95 100 105

Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala
110 115 120

Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg
125 130 135

Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
140 145 150

Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp
155 160 165

Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala
170 175 180

Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly
185 190 195

His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu
200 205 210

Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser
215 220 225

Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu
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<210> 41
<211> 334
<212> PRT
<213> Homo sapiens
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<400>	41													
Met	Leu	Ala	Leu	Ala	Lys	Ile	Leu	Leu	Ile	Ser	Thr	Leu	Phe	Tyr
1				5					10					15
Ser	Leu	Leu	Ser	Gly	Ser	His	Gly	Lys	Glu	Asn	Gln	Asp	Ile	Asn
				20					25					30
Thr	Thr	Gln	Asn	Ile	Ala	Glu	Val	Phe	Lys	Thr	Met	Glu	Asn	Lys
				35					40					45
Pro	Ile	Ser	Leu	Glu	Ser	Glu	Ala	Asn	Leu	Asn	Ser	Asp	Lys	Glu
				50					55					60
Asn	Ile	Thr	Thr	Ser	Asn	Leu	Lys	Ala	Ser	His	Ser	Pro	Pro	Leu
				65					70					75
Asn	Leu	Pro	Asn	Asn	Ser	His	Gly	Ile	Thr	Asp	Phe	Ser	Ser	Asn
				80					85					90
Ser	Ser	Ala	Glu	His	Ser	Leu	Gly	Ser	Leu	Lys	Pro	Thr	Ser	Thr
				95					100					105
Ile	Ser	Thr	Ser	Pro	Pro	Leu	Ile	His	Ser	Phe	Val	Ser	Lys	Val
				110					115					120
Pro	Trp	Asn	Ala	Pro	Ile	Ala	Asp	Glu	Asp	Leu	Leu	Pro	Ile	Ser
				125					130					135
Ala	His	Pro	Asn	Ala	Thr	Pro	Ala	Leu	Ser	Ser	Glu	Asn	Phe	Thr
				140					145					150
Trp	Ser	Leu	Val	Asn	Asp	Thr	Val	Lys	Thr	Pro	Asp	Asn	Ser	Ser
				155					160					165
Ile	Thr	Val	Ser	Ile	Leu	Ser	Ser	Glu	Pro	Thr	Ser	Pro	Ser	Val
				170					175					180
Thr	Pro	Leu	Ile	Val	Glu	Pro	Ser	Gly	Trp	Leu	Thr	Thr	Asn	Ser
				185					190					195

Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu	
				200					205					210	
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn	
				215					220					225	
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe	
				230					235					240	
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu	
				245					250					255	
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser	
				260					265					270	
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu	
				275					280					285	
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser	
				290					295					300	
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu	
				305					310					315	
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu	
				320					325					330	

Arg Thr Ser Val

<210> 42
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<400> 42
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 cccctaccgc cgtgcaaaag gaggaggcgc ggcaagacgt ggaggccctc 150
 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200
 tgccacccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250
 taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300
 tacaagtact tcatgcccaa gagcaccatt taccgtggag agatgtgctt 350
 ttttgattct gaggatcctg caaattccct tcgtggagga gagcctaact 400
 tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450
 atcattgatg tgcctgtccc cagtttctct gatagtgacc ctgcagcaat 500
 tattcatgac ttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550

ggaactgcta tctgatgcc ctcaatactt ctattgttat gcctccaaaa 600
aatctggtag agctcttttg caaactggcg agtggcagat atctgcctca 650
aacttatgtg gttcgagaag acctagtgtc tgtggaggaa attcgtgatg 700
ttagtaacct tggcatcttt atttaccaac ttgcaataa cagaaagtcc 750
ttccgccttc gtcgcagaga cctcttgctg ggtttcaaca aacgtgccat 800
tgataaatgc tggaagatta gacacttccc caacgaattt attgttgaga 850
ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtaata 900
agaagtcaga gatttacaat atgactttta cattaagggt tatgggatac 950
tcaagatatt tactcatgca ttactctat tgcttatgct ttaaaaaaag 1000
gaaaaaaaa aaaactacta accactgcaa gctcttgtca aatttttagtt 1050
taattggcat tgcttgTTTT ttgaaactga aattacatga gtttcatttt 1100
ttctttgcat ttatagggtt tagatttctg aaagcagcat gaatatatca 1150
cctaacatcc tgacaataaa ttccatccgt tgTTTTTTTT gtttgTTTgt 1200
TTTTTctttt cctttaagta agctctttat tcactttatg gtggagcaat 1250
tttaaaattt gaaatatttt aaattgtttt tgaacttttt gtgtaaaata 1300
tatcagatct caacattggt ggTTTTTTTT gTTTTtcatt ttgtacaact 1350
ttcttgaatt tagaaattac atctttgcag ttctgttagg tgctctgtaa 1400
ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450
aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500
tgtgtagggt ctgaatgctg taaggagttt aggttgtagt aattctacaa 1550
ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43
<211> 263
<212> PRT
<213> Homo sapiens

<400> 43
Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu
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Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg
20 25 30
Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
35 40 45
Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

50	55	60
Ser Phe Ile Leu Ala Gly Leu Ile Val	Gly Gly Ala Cys Ile Tyr	
65	70	75
Lys Tyr Phe Met Pro Lys Ser Thr Ile	Tyr Arg Gly Glu Met Cys	
80	85	90
Phe Phe Asp Ser Glu Asp Pro Ala Asn	Ser Leu Arg Gly Gly Glu	
95	100	105
Pro Asn Phe Leu Pro Val Thr Glu Glu	Ala Asp Ile Arg Glu Asp	
110	115	120
Asp Asn Ile Ala Ile Ile Asp Val Pro	Val Pro Ser Phe Ser Asp	
125	130	135
Ser Asp Pro Ala Ala Ile Ile His Asp	Phe Glu Lys Gly Met Thr	
140	145	150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn	Cys Tyr Leu Met Pro Leu	
155	160	165
Asn Thr Ser Ile Val Met Pro Pro Lys	Asn Leu Val Glu Leu Phe	
170	175	180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu	Pro Gln Thr Tyr Val Val	
185	190	195
Arg Glu Asp Leu Val Ala Val Glu Glu	Ile Arg Asp Val Ser Asn	
200	205	210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys	Asn Asn Arg Lys Ser Phe	
215	220	225
Arg Leu Arg Arg Arg Asp Leu Leu Leu	Gly Phe Asn Lys Arg Ala	
230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His	Phe Pro Asn Glu Phe Ile	
245	250	255
Val Glu Thr Lys Ile Cys Gln Glu		
260		

<210> 44
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 44
 gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-20
<223> Synthetic construct.

<400> 45
gggaactgct atctgatgcc 20

<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
caggatctcc tcttgcatgc tgcagc 26

<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-28
<223> Synthetic construct.

<400> 47
cttctcgaac cacataagtt tgaggcag 28

<210> 48
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 48
cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<400> 49
ggaggagggga gggcgggcag ggcagccc agagcagccc cgggcaccag 50

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cgggagcacc	cagtcctgta	cgccaaggaa	ctggctcctgg	gggcaccatg	150
gtttcggcgg	cagccccag	cctcctcatc	cttctgttgc	tgtctgtggg	200
gtctgtgcct	gctaccgacg	cccgtcttgt	gcccctgaag	gccacgttcc	250
tggaggatgt	ggcgggtagt	ggggaggccg	agggctcgtc	ggcctcctcc	300
ccgagcctcc	cgccaccctg	gaccccggcc	ctcagcccca	catcgatggg	350
gccccagccc	acaaccctgg	ggggcccatc	acccccacc	aacttcctgg	400
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ggctccctgg	cctttctgct	gatgttcac	gtctgtgccg	cggtcatcac	500
ccggcagaag	cagaaggcct	cggcctatta	cccatcgtcc	ttccccaaga	550
agaagtacgt	ggaccagagt	gaccggggccg	ggggcccccg	ggccttcagt	600
gaggtccccg	acagagcccc	cgacagcagg	cccaggaag	ccctggattc	650
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agtccaggga	catggggctc	cagtggagac	accagaggcg	caggaggagc	850
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ccccgtgtat	gaaaaggcct	tcagccctga	ctgcttcctg	acactccctc	1100
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cagaaatgct	ggtccccggt	gccccggagg	aatcttacca	agtgccatca	1200
tccttcacct	cagcagcccc	aaagggctac	atcctacagc	acagctcccc	1250
tgacaaagtg	agggagggca	cgtgtccctg	tgacagccag	gataaaacat	1300
cccccaaagt	gctgggatta	caggcgtgag	ccaccgtgcc	cggcccaaac	1350
tactttttaa	aacagctaca	gggtaaaatc	ctgcagcacc	cactctggaa	1400
aatactgctc	ttaattttcc	tgaaggtggc	cccctgtttc	tagttggtcc	1450
aggattaggg	atgtggggta	tagggcattt	aaatcctctc	aagcgctctc	1500

Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr
170 175 180

Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp
185 190 195

Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Glu Lys
200 205 210

Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro
215 220 225

Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu
230 235 240

Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly
245 250 255

Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro
260 265 270

Glu Ser Pro Cys Ala Cys Ser Ser Val His Pro Ser Val
275 280

<210> 51
<211> 1734
<212> DNA
<213> Homo sapiens

<400> 51
gtggactctg agaagcccag gcagttgagg acaggagaga gaaggctgca 50
gaccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100
gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150
agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200
cctggcctgc ctctgctgg ccctctgcct gggcagtggg gaggctggcc 250
ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300
ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg 350
caaagaggcc ggaggggcag ctggctctaa agtcagttag gcccttggcc 400
aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt 450
ggcgagcag atgctttggg caacagggtc ggggaagcag cccatgctct 500
gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550
acggagcaga tgctgtccgc ggctcctggc aggggggtgcc tggccacagt 600
ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaaggtgg 650
ccttgagggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700

tccacggata ccccggaac tcagcaggca gctttggaat gaatcctcag 750
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 ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtgg 950
 cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000
 gcagtggcag cagcagtggc agcagcagtg gcggcagcag tggcggcagc 1050
 agtgggtggca gcagtggcaa cagtgggtggc agcagaggtg acagcggcag 1100
 tgagtcctcc tggggatcca gcaccggctc ctctccggc aaccacggtg 1150
 ggagcggcgg aggaaatgga cataaaccgg ggtgtgaaaa gccagggaat 1200
 gaagcccgcg ggagcgggga atctgggatt cagggttca gaggacaggg 1250
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 gaggctctgg agacaattat cgggggcaag ggtcgagctg gggcagtgga 1350
 ggaggtgacg ctgttggtgg agtcaatact gtgaactctg agacgtctcc 1400
 tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450
 gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcatc 1500
 ccgtgacctc cagacaagga gccaccagat tggatgggag cccccacact 1550
 ccctccttaa aacaccaccc tctcatcact aatctcagcc cttgcccttg 1600
 aaataaacct tagctgcccc acaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52
 <211> 440
 <212> PRT
 <213> Homo sapiens

<400> 52
 Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys
 1 5 10 15
 Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser
 20 25 30
 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
 35 40 45
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

50	55	60
Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr		
65	70	75
Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly		
80	85	90
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala		
95	100	105
Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val		
110	115	120
Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val		
125	130	135
Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile		
140	145	150
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro		
155	160	165
Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser		
170	175	180
Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln		
185	190	195
Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly		
200	205	210
Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln		
215	220	225
Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly		
230	235	240
Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser		
245	250	255
Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly		
260	265	270
Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser		
275	280	285
Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser		
290	295	300
Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly		
305	310	315
Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His		
320	325	330
Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly		
335	340	345

gagttctgtc	aaaggaagag	ccctgggggt	gtgcggg'gcgc	tgcttccaga	850
ggagacccccg	gcagccgttc	tgagcagtgc	agagaacatt	gctgtggggc	900
ttgcaacaga	gaaagcctgt	gcttggctgt	cagccaacat	cacagcactg	950
atcaggagggg	aggtgaaagc	agcagtgagt	cgcacacttc	gagcccaggg	1000
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gtgctctcct	tggccgtggg	gccacgggac	cctgacgagg	gagtctcccc	1100
agagcatctg	gaacagctcc	taggccagct	gggccagacg	ctgcgggtgcc	1150
gccagttcct	gtgcccacct	gctgagcagc	atctggcaaa	gtgctctgtg	1200
gagttagctt	ccctcctcgt	tgcagatcaa	attcctatcc	tagggccccc	1250
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cagctgtggc	cggtgctcct	tcytaggcc	gtcctgggga	aactaagctc	3000
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cagcggcctg	gagcgcctct	ctcctgagcc	tcagtttccc	tttccgtcta	3150
atgaagaaca	tgccgtctcg	gtgtctcagg	gctattagga	cttgccctca	3200
ggaagtggcc	ttggacgagc	gtcatgttat	tttcacaact	gtcctgcgac	3250
gttggcctgg	gcacgtcatg	gaatggccca	tgtccctctg	ctgcgtggac	3300
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gcccttgatg	cagtgcggca	gcgcgtcgtc	cgccagctgg	aagcagcgcc	3550
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```
<210> 54
<211> 280
<212> PRT
<213> Homo sapiens
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<400> 54

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Leu	Phe	Gln	Ile	Pro	Thr	Val	Pro	Glu	Asp	Leu	Phe	Phe	Leu	Glu
				20					25					30
Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Glu	Val	Asp	Thr	Val	Ala	Pro	Glu
				35					40					45
His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
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Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
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Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
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Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln
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Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
				110					115					120
Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu
				125					130					135
Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val
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Ala	Asp	Leu	Val	Arg	Gln	Ala	Glu	Ser	Leu	Leu	Gln	Glu	Gln	Leu
				155					160					165
Val	Thr	Gln	Gly	Glu	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu
				170					175					180
Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala
				185					190					195
Leu	Gly	Arg	Glu	Phe	Cys	Gln	Arg	Lys	Ser	Pro	Gly	Ala	Val	Arg
				200					205					210
Ala	Leu	Leu	Pro	Glu	Glu	Thr	Pro	Ala	Ala	Val	Leu	Ser	Ser	Ala
				215					220					225
Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp
				230					235					240
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala
				245					250					255
Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala
				260					265					270
Arg	Gly	Glu	Arg	Arg	Gly	Cys	Ser	Arg	Ala					
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<210> 55
<211> 2401
<212> DNA
<213> Homo sapiens

<400> 55
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<210> 56
<211> 299
<212> PRT
<213> Homo sapiens

<400> 56
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Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro	
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Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val	
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Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro	
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Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro	
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Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg	
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Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln	
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Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly	
				140					145					150	
Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val	
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Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala	
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Val	Ser	Pro	Gly	Arg	Met	Arg	Gln	Phe	Asp	Asp	Leu	Phe	Arg	Gly	
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Glu	Thr	Gly	Lys	Asp	Arg	Glu	Lys	Ser	His	Ser	Trp	Leu	Ser	Thr	
				200					205					210	
Gly	Trp	Phe	Thr	Met	Val	Ile	Ala	Val	Glu	Leu	Cys	Asp	His	Val	
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His	Val	Tyr	Gly	Met	Val	Pro	Pro	Asn	Tyr	Cys	Ser	Gln	Arg	Pro	
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Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro	
				245					250					255	
Asp	Glu	Cys	Val	Thr	Tyr	Ile	Gln	Asn	Glu	His	Ser	Arg	Lys	Gly	
				260					265					270	
Asn	His	His	Arg	Phe	Ile	Thr	Glu	Lys	Arg	Val	Phe	Ser	Ser	Trp	
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<210> 57

<211> 4277

<212> DNA

<213> Homo sapiens

<400> 57

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<210> 58
 <211> 1115

<212> PRT
 <213> Homo sapiens

<400> 58

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Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr	35	40	45	
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	50	55	60	
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu	65	70	75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	80	85	90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	95	100	105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	110	115	120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	125	130	135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	140	145	150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	155	160	165	
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	170	175	180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	185	190	195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	200	205	210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	215	220	225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	230	235	240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	245	250	255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	260	265	270	

Val Thr Gly Tyr	Asn Lys Thr Arg Phe	Leu Leu Ser Asn Leu Leu	275	280	285
Ile Asp Thr Thr	Ser Glu Glu Asp Ser	Gly Thr Tyr Arg Cys Met	290	295	300
Ala Asp Asn Gly	Val Gly Gln Pro Gly	Ala Ala Val Ile Leu Tyr	305	310	315
Asn Val Gln Val	Phe Glu Pro Pro Glu	Val Thr Met Glu Leu Ser	320	325	330
Gln Leu Val Ile	Pro Trp Gly Gln Ser	Ala Lys Leu Thr Cys Glu	335	340	345
Val Arg Gly Asn	Pro Pro Pro Ser Val	Leu Trp Leu Arg Asn Ala	350	355	360
Val Pro Leu Ile	Ser Ser Gln Arg Leu	Arg Leu Ser Arg Arg Ala	365	370	375
Leu Arg Val Leu	Ser Met Gly Pro Glu	Asp Glu Gly Val Tyr Gln	380	385	390
Cys Met Ala Glu	Asn Glu Val Gly Ser	Ala His Ala Val Val Gln	395	400	405
Leu Arg Thr Ser	Arg Pro Ser Ile Thr	Pro Arg Leu Trp Gln Asp	410	415	420
Ala Glu Leu Ala	Thr Gly Thr Pro Pro	Val Ser Pro Ser Lys Leu	425	430	435
Gly Asn Pro Glu	Gln Met Leu Arg Gly	Gln Pro Ala Leu Pro Arg	440	445	450
Pro Pro Thr Ser	Val Gly Pro Ala Ser	Pro Lys Cys Pro Gly Glu	455	460	465
Lys Gly Gln Gly	Ala Pro Ala Glu Ala	Pro Ile Ile Leu Ser Ser	470	475	480
Pro Arg Thr Ser	Lys Thr Asp Ser Tyr	Glu Leu Val Trp Arg Pro	485	490	495
Arg His Glu Gly	Ser Gly Arg Ala Pro	Ile Leu Tyr Tyr Val Val	500	505	510
Lys His Arg Lys	Gln Val Thr Asn Ser	Ser Asp Asp Trp Thr Ile	515	520	525
Ser Gly Ile Pro	Ala Asn Gln His Arg	Leu Thr Leu Thr Arg Leu	530	535	540
Asp Pro Gly Ser	Leu Tyr Glu Val Glu	Met Ala Ala Tyr Asn Cys	545	550	555
Ala Gly Glu Gly	Gln Thr Ala Met Val	Thr Phe Arg Thr Gly Arg			

560										565					570					
Arg	Pro	Lys	Pro	Glu	Ile	Met	Ala	Ser	Lys	Glu	Gln	Gln	Ile	Gln						
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Arg	Asp	Asp	Pro	Gly	Ala	Ser	Pro	Gln	Ser	Ser	Ser	Ser	Gln	Pro	Asp					
				590					595					600						
His	Gly	Arg	Leu	Ser	Pro	Pro	Glu	Ala	Pro	Asp	Arg	Pro	Thr	Ile						
				605					610					615						
Ser	Thr	Ala	Ser	Glu	Thr	Ser	Val	Tyr	Val	Thr	Trp	Ile	Pro	Arg						
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Lys	Leu	Lys	Lys	Val	Gly	Asp	Trp	Ile	Leu	Ala	Thr	Ser	Ala	Ile						
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Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly						
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Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu						
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Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr						
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Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr						
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Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr						
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Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro						
				815					820					825						
Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg						
				830					835					840						
Pro	Val	Gly	Thr	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro						
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[illegible]

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<210> 59
<211> 25
<212> DNA
<213> Artificial
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<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

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<210> 60
<211> 24
<212> DNA
<213> Artificial
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<222> 1-24  
<223> Synthetic construct.
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<210> 61
<211> 42
<212> DNA
<213> Artificial
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<220>
<221> Artificial sequence
<222> 1-42
<223> Synthetic construct.

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<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens
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<221> unsure
<222> 678
<223> unknown base
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cacggggccgc gaggggtccc gcgcgctcag ccggcggtat ctgcggcgctc 150
tgctgctcct gctactgctg ctgctgctgc ggcagcccggt aaccgcgcgcg 200
gagaccacgc cgggcgcccc cagagccctc tccacgctgg gctccccacg 250
cctcttcacc acgccgggtg tccccagcgc cctcactacc ccaggcctca 300
ctacgccagg ccccccaaaa accctggacc ttcggggctcg cgcgcaggcc 350
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ctgatgcgga	gtttcccaact	cgtggacggc	cacaatgacc	tgccccaggt	400
cctgagacag	cgttacaaga	atgtgcttca	ggatgttaac	ctgcgaaatt	450
tcagccatgg	tcagaccagc	ctggacaggc	ttagagacgg	cctcgtgggt	500
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<210> 63
<211> 487
<212> PRT
<213> Homo sapiens
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<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63

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Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	
				20					25					30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	
				35					40					45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	
				50					55					60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	
				65					70					75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	
				80					85					90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	
				95					100					105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	
				110					115					120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	
				125					130					135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	
				140					145					150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	
				155					160					165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	
				170					175					180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	
				185					190					195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	
				200					205					210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	
				215					220					225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	
				230					235					240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	
				245					250					255	
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<210> 65
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 65
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<210> 66
 <211> 47
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-47
 <223> Synthetic construct.

<400> 66
 ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67
 <211> 1564
 <212> DNA
 <213> Homo sapiens

<400> 67
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 aacaccacaca gatccctcta tgactgcaat gtgaggtgtc cggctttgct 100
 ggcccagcaa gcctgataag catgaagctc ttatctttgg tggctgtggt 150
 cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
 tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250
 tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300
 gcccatgcc a gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350
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 gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500
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ctccttctcc	ctaactttag	aaatgttgta	cttggtatt	ttgattagg	850
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<210> 68
<211> 183
<212> PRT
<213> Homo sapiens
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Pro  Pro  Ala  Glu  Ala  Asn  Lys  Ser  Ser  Glu  Asp  Ile  Arg  Cys  Lys
              20              25              30

Cys  Ile  Cys  Pro  Pro  Tyr  Arg  Asn  Ile  Ser  Gly  His  Ile  Tyr  Asn
              35              40              45

Gln  Asn  Val  Ser  Gln  Lys  Asp  Cys  Asn  Cys  Leu  His  Val  Val  Glu
              50              55              60

```

Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu
65 70 75

Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val
80 85 90

Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr
95 100 105

Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
110 115 120

Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala
125 130 135

Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
140 145 150

Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
155 160 165

Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys
170 175 180

Met Leu Ser

<210> 69
<211> 3170
<212> DNA
<213> Homo sapiens

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 aaaacttttt cgtttgttca ggttttggca acacatagat catatgtctg 2100

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gcagaatata	tttgcagcta	ttgactttgt	aatttaggaa	aaatgtataa	3100
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aaaaaaaaaa	aaaaaaaaaa	3170			

<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

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Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser
20 25 30

Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu
35 40 45

[illegible]

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<210> 71
<211> 1809
<212> DNA
<213> Homo sapiens
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acatcacggtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150
cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200
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aaaatacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350
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 gccgggtgtg gtggcggcgc gtgcctgtaa tcccagctac ttgggaggct 1750
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 ctgaaaaga 1809

<210> 72
 <211> 363
 <212> PRT
 <213> Homo sapiens

<400> 72
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 35 40 45
 Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
 50 55 60
 Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
 65 70 75
 Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
 80 85 90
 Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
 95 100 105
 Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
 110 115 120
 Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
 125 130 135
 Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
 140 145 150
 Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
 155 160 165
 Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
 170 175 180
 Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
 185 190 195
 Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
 200 205 210
 Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
 215 220 225

Ser Ser Glu Asn	Ser Asn Gln Ile Pro	Ile Ser Leu Tyr Ser	Lys
230		235	240
Ser Leu Ser Glu	Pro Leu Asn Thr Ser	Leu Ser Met Thr Ser	Ala
245		250	255
Val Gln Asn Ser	Thr Tyr Thr Thr Ser	Val Ile Thr Ser Cys	Ser
260		265	270
Leu Thr Ser Ser	Ser Leu Asn Ser Ala	Ser Pro Val Ala Met	Ser
275		280	285
Ser Ser Tyr Asp	Gln Ser Ser Val His	Asn Arg Ile Pro Tyr	Gln
290		295	300
Ser Pro Val Ser	Ser Ser Glu Ser Ala	Pro Gly Thr Ile Met	Asn
305		310	315
Gly His Gly Gly	Gly Arg Ser Gln Gln	Thr Leu Asp Ser Lys	Tyr
320		325	330
Ser Ser Lys Leu	Leu Leu Ser Trp Leu	Val Pro Thr Lys Gln	Arg
335		340	345
Lys Arg Ile Ala	His Val Met Trp Lys	Thr Pro Val Gly Gln	Trp
350		355	360

Leu Ile Arg

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 73
 aattcatggc aaatatttcc cttccc 26

<210> 74
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 74
 tggtaaactg gcccaaactc gg 22

<210> 75
 <211> 50

<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
ttaaagtcac cgcctcttgg ctcaggattt ggagagcttg caccaccaa 50

<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
gccgagtggg acaaagcctg gggctgggcg ggggccatgg cgctgccatc 50
ccgaatcctg ctttggaac ttgtgttct gcagagctct gctgttctcc 100
tgactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150
caccatcact actgccact ctacgagagc ctggccgtcc gcctggagggt 200
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 caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77
 <211> 341
 <212> PRT
 <213> Homo sapiens

<400> 77
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 Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp
 20 25 30
 Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
 35 40 45
 Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
 50 55 60
 Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
 65 70 75

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<210> 79
<211> 475
<212> PRT
<213> Homo sapiens

<400> 79
Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser
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Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg
35 40 45
Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu
50 55 60
Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys
65 70 75
Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr
80 85 90
Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser
95 100 105

Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val
				110					115					120
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val
				125					130					135
Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr
				140					145					150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe
				155					160					165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr
				170					175					180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met
				185					190					195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr
				200					205					210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp
				215					220					225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe
				230					235					240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu
				245					250					255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe
				260					265					270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser
				275					280					285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro
				290					295					300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val
				305					310					315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile
				320					325					330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe
				335					340					345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu
				350					355					360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn
				365					370					375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile
				380					385					390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys

395	400	405
Thr Val Val Phe Gln Ser Asp Val Tyr	Pro Ala Leu Leu Ser Ser	
410	415	420
Leu Leu Gly Leu Ser Asn Gly Tyr Leu	Ser Thr Leu Ala Leu Leu	
425	430	435
Tyr Gly Pro Lys Ile Val Pro Arg Glu	Leu Ala Glu Ala Thr Gly	
440	445	450
Val Val Met Ser Phe Tyr Val Cys Leu	Gly Leu Thr Leu Gly Ser	
455	460	465
Ala Cys Ser Thr Leu Leu Val His Leu	Ile	
470	475	

<210> 80
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 80
 ttttgcggtc accattgtct gc 22

<210> 81
 <211> 23
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Artificial sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 81
 cgtaggtgac acagaagccc agg 23

<210> 82
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-49
 <223> Synthetic construct.

<400> 82
 tacggcatga ccggtcctt tcctatgagg aactcccagg cactgatat 49

<210> 83
 <211> 1844

10017834 121291

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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84
 <211> 567
 <212> PRT
 <213> Homo sapiens

<400> 84
 Met Ala Pro Leu Ala Leu His Leu Leu Val Leu Val Pro Ile Leu
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 Leu Ser Leu Val Ala Ser Gln Asp Trp Lys Ala Glu Arg Ser Gln
 20 25 30
 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu
 35 40 45
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
 50 55 60
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
 65 70 75
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
 80 85 90
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
 95 100 105
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
 110 115 120
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
 125 130 135
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
 140 145 150
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
 155 160 165

Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu
170 175 180

Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys
185 190 195

Ala Leu Gly Cys Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr
200 205 210

Leu Leu Glu Tyr Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala
215 220 225

Val Gln Leu Leu Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr
230 235 240

Leu Ser Phe Ala Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp
245 250 255

Arg Leu Gln Tyr Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro
260 265 270

Arg Ala Leu Leu Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala
275 280 285

Pro Val Val Ala Met Thr Gln Gly Pro His Asp Val His Val Gln
290 295 300

Ile Glu Thr Ser Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala
305 310 315

Asp Val Val Leu Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile
320 325 330

Thr Phe Ser Pro Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg
335 340 345

Arg Leu His Tyr Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg
350 355 360

Arg Pro Phe Trp Arg Glu Glu His Ile Glu Gly Gly His Ser Asn
365 370 375

Thr Asp Arg Pro Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu
380 385 390

Gly Ala Leu Leu Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala
395 400 405

Ala Phe Ala Gly Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu
410 415 420

Asp Asp Val Ala Ala Leu His Gly Pro Val Val Arg Gln Leu Trp
425 430 435

Asp Gly Thr Gly Val Val Lys Arg Trp Ala Glu Asp Gln His Ser
440 445 450

Gln Gly Gly Phe Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu

455	460	465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly		
470	475	480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys		
485	490	495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro		
500	505	510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu		
515	520	525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp		
530	535	540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu		
545	550	555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His		
560	565	

<210> 85
 <211> 3316
 <212> DNA
 <213> Homo sapiens

<400> 85
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 agataacaca tggtgtttct acttgtaaatt gtaaagtctt taaaataaac 3300
 tattacagat aaaaaa 3316

<210> 86
 <211> 739
 <212> PRT
 <213> Homo sapiens

<400> 86
 Met Asp Ala Leu Lys Pro Pro Cys Leu Trp Arg Asn His Glu Arg
 1 5 10 15
 Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro
 20 25 30

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser	35	40	45
Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile	50	55	60
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys	65	70	75
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg	80	85	90
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val	95	100	105
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn	110	115	120
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu	125	130	135
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu	140	145	150
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys	155	160	165
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His	170	175	180
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala	185	190	195
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr	200	205	210
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu	215	220	225
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile	230	235	240
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu	245	250	255
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro	260	265	270
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu	275	280	285
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe	290	295	300
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys	305	310	315
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr			

320										325					330				
His	Gln	Asn	Ile	Val	Ser	Asn	Ala	Ala	Ala	Phe	Leu	Lys	Cys	Val					
				335					340					345					
Glu	His	Ala	Tyr	Glu	Pro	Thr	Pro	Asp	Asp	Val	Ala	Ile	Ser	Tyr					
				350					355					360					
Leu	Pro	Leu	Ala	His	Met	Phe	Glu	Arg	Ile	Val	Gln	Ala	Val	Val					
				365					370					375					
Tyr	Ser	Cys	Gly	Ala	Arg	Val	Gly	Phe	Phe	Gln	Gly	Asp	Ile	Arg					
				380					385					390					
Leu	Leu	Ala	Asp	Asp	Met	Lys	Thr	Leu	Lys	Pro	Thr	Leu	Phe	Pro					
				395					400					405					
Ala	Val	Pro	Arg	Leu	Leu	Asn	Arg	Ile	Tyr	Asp	Lys	Val	Gln	Asn					
				410					415					420					
Glu	Ala	Lys	Thr	Pro	Leu	Lys	Lys	Phe	Leu	Leu	Lys	Leu	Ala	Val					
				425					430					435					
Ser	Ser	Lys	Phe	Lys	Glu	Leu	Gln	Lys	Gly	Ile	Ile	Arg	His	Asp					
				440					445					450					
Ser	Phe	Trp	Asp	Lys	Leu	Ile	Phe	Ala	Lys	Ile	Gln	Asp	Ser	Leu					
				455					460					465					
Gly	Gly	Arg	Val	Arg	Val	Ile	Val	Thr	Gly	Ala	Ala	Pro	Met	Ser					
				470					475					480					
Thr	Ser	Val	Met	Thr	Phe	Phe	Arg	Ala	Ala	Met	Gly	Cys	Gln	Val					
				485					490					495					
Tyr	Glu	Ala	Tyr	Gly	Gln	Thr	Glu	Cys	Thr	Gly	Gly	Cys	Thr	Phe					
				500					505					510					
Thr	Leu	Pro	Gly	Asp	Trp	Thr	Ser	Gly	His	Val	Gly	Val	Pro	Leu					
				515					520					525					
Ala	Cys	Asn	Tyr	Val	Lys	Leu	Glu	Asp	Val	Ala	Asp	Met	Asn	Tyr					
				530					535					540					
Phe	Thr	Val	Asn	Asn	Glu	Gly	Glu	Val	Cys	Ile	Lys	Gly	Thr	Asn					
				545					550					555					
Val	Phe	Lys	Gly	Tyr	Leu	Lys	Asp	Pro	Glu	Lys	Thr	Gln	Glu	Ala					
				560					565					570					
Leu	Asp	Ser	Asp	Gly	Trp	Leu	His	Thr	Gly	Asp	Ile	Gly	Arg	Trp					
				575					580					585					
Leu	Pro	Asn	Gly	Thr	Leu	Lys	Ile	Ile	Asp	Arg	Lys	Lys	Asn	Ile					
				590					595					600					
Phe	Lys	Leu	Ala	Gln	Gly	Glu	Tyr	Ile	Ala	Pro	Glu	Lys	Ile	Glu					
				605					610					615					

Asn	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His
				620						625				630
Gly	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Val	Gly	Val	Val	Val	Pro	Asp
				635						640				645
Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
				650						655				660
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
				665						670				675
Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
				680						685				690
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
				695						700				705
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
				710						715				720
Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu
				725						730				735

His Ile Gln Asp

<210> 87
 <211> 2725
 <212> DNA
 <213> Homo sapiens

<400> 87
 ggaggcggag gccgcggcga gccggggccga gcagtgaggg ccctagcggg 50
 gcccgagcgg ggcccggggc ccctaagcca ttctgaagt catgggctgg 100
 ccaggacatt ggtgaccgc caatccgta tggacgactg gaagcccagc 150
 cccctcatca agccctttgg ggctcggaag aagcggagct ggtaccttac 200
 ctggaagtat aaactgaaa accagcgggc cctgcggaga ttctgtcaga 250
 caggggccgt gcttttcctg ctggtgactg tcattgtcaa tatcaagttg 300
 atcctggaca ctggcgagc catcagtga gccaatgaag acccagagcc 350
 agagcaagac tatgatgagg ccctaggccg cctggagccc ccacggcgca 400
 gaggcagtgg tccccggcg gtctggagc tagaggtgta ttcaagtcgc 450
 agcaaagtat atgtggcagt ggatggcacc acggtgctgg aggatgaggc 500
 ccgggagcag ggccggggca tccatgtcat tgtcctcaac caggccacgg 550
 gccacgtgat ggcaaacgt gtgtttgaca cgtactcacc tcatgaggat 600
 gaggccatgg tgctattcct caacatgta gcgcccggcc gagtgctcat 650

ctgcactgtc aaggatgagg gtccttcca cctcaaggac acagccaagg 700
ctctgctgag gagcctgggc agccaggctg gccctgccct gggctggagg 750
gacacatggg ccttcgtggg acgaaaagga ggtcctgtct tcggggagaa 800
acattctaag tcacctgccc tctcttctg gggggaccca gtctgtgta 850
agacagatgt gccattgagc tcagcagaag aggcagagtg cactgggca 900
gacacagagc tgaaccgtcg ccgccggcgc ttctgcagca aagttgaggg 950
ctatggaagt gtatgcagct gcaaggaccc cacaccatc gagttcagcc 1000
ctgaccact cccagacaac aaggtcctca atgtgcctgt ggctgtcatt 1050
gcagggaacc gacccaatta cctgtacagg atgtgcgct ctctgctttc 1100
agcccagggg gtgtctctc agatgataac agttttcatt gacggctact 1150
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cactactcca tcagcatcaa gaatgccgc gtgtctcagc actacaaggc 1250
cagcctcact gccactttca acctgtttcc ggaggccaag tttgctgtgg 1300
ttctggaaga ggacctggac attgctgtgg attttttcag tttcctgagc 1350
caatccatcc acctactgga ggaggatgac agcctgtact gcatctctgc 1400
ctggaatgac caggggtatg aacacacggc tgaggacca gcactactgt 1450
accgtgtgga gaccatgcct gggctgggct gggtgctcag gaggtccttg 1500
tacaaggagg agcttgagcc caagtggcct acaccgaaa agctctggga 1550
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tcatccctga cgtttccga tctaccact ttggcatcgt cggcctcaac 1650
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ggttccaggt gtccagctca ggaatgtgga cagtctgaag aaagaagctt 1750
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agcaagaacc cttgtgaaga ctctttctg ccagacacag agggccacac 1850
ctacgtggcc ttattogaa tggagaaaga tgatgacttc accacctgga 1900
cccagcttgc caagtgcctc catatctggg acctggatgt gcgtggcaac 1950
catcggggcc tgtggagatt gtttcggaag aagaaccact tcctggtggt 2000
gggggtcccg gcttccccct actcagtga gaagccacc tcagtcacc 2050
caattttcct ggagccaccc ccaaaggagg agggagcccc aggagcccca 2100

gaacagacat gagacctcct ccaggaccct gcggggctgg gtactgtgta 2150
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 cctgaggggtg gggctggctc ttactcagga aactgctgtg cccaacccat 2550
 ggacaggccc agctggggcc cacatgctga cacagactca ctcagagacc 2600
 cttagacact ggaccaggcc tcctctcagc cttctctttg tccagatttc 2650
 caaagctgga taagttggctc attgattaaa aaaggagaag ccctctggga 2700
 aaaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88
 <211> 660
 <212> PRT
 <213> Homo sapiens

<400> 88
 Met Asp Asp Trp Lys Pro Ser Pro Leu Ile Lys Pro Phe Gly Ala
 1 5 10 15
 Arg Lys Lys Arg Ser Trp Tyr Leu Thr Trp Lys Tyr Lys Leu Thr
 20 25 30
 Asn Gln Arg Ala Leu Arg Arg Phe Cys Gln Thr Gly Ala Val Leu
 35 40 45
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
 50 55 60
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
 65 70 75
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
 80 85 90
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
 95 100 105
 Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
 110 115 120
 Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
 125 130 135

Leu Asn Gln Ala Thr Gly His Val Met	Ala Lys Arg Val Phe Asp	140	145	150
Thr Tyr Ser Pro His Glu Asp Glu Ala Met	Val Leu Phe Leu Asn	155	160	165
Met Val Ala Pro Gly Arg Val Leu Ile Cys	Thr Val Lys Asp Glu	170	175	180
Gly Ser Phe His Leu Lys Asp Thr Ala Lys	Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly	Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val	Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly	Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu	Glu Ala Glu Cys His	245	250	255
Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg	Arg Arg Arg Phe Cys Ser	260	265	270
Lys Val Glu Gly Tyr Gly Ser Val Cys Ser	Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro	Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly Asn	Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala	Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr	Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly	Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln	His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu	Ala Lys Phe Ala Val	380	385	390
Val Leu Glu Glu Asp Leu Asp Ile Ala Val	Asp Phe Phe Ser Phe	395	400	405
Leu Ser Gln Ser Ile His Leu Leu Glu Glu	Asp Asp Ser Leu Tyr	410	415	420
Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr	Glu His Thr Ala Glu			

425	430	435
Asp Pro Ala Leu Leu Tyr Arg Val Glu	Thr Met Pro Gly Leu Gly	
440	445	450
Trp Val Leu Arg Arg Ser Leu Tyr Lys	Glu Glu Leu Glu Pro Lys	
455	460	465
Trp Pro Thr Pro Glu Lys Leu Trp Asp	Trp Asp Met Trp Met Arg	
470	475	480
Met Pro Glu Gln Arg Arg Gly Arg Glu	Cys Ile Ile Pro Asp Val	
485	490	495
Ser Arg Ser Tyr His Phe Gly Ile Val	Gly Leu Asn Met Asn Gly	
500	505	510
Tyr Phe His Glu Ala Tyr Phe Lys Lys	His Lys Phe Asn Thr Val	
515	520	525
Pro Gly Val Gln Leu Arg Asn Val Asp	Ser Leu Lys Lys Glu Ala	
530	535	540
Tyr Glu Val Glu Val His Arg Leu Leu	Ser Glu Ala Glu Val Leu	
545	550	555
Asp His Ser Lys Asn Pro Cys Glu Asp	Ser Phe Leu Pro Asp Thr	
560	565	570
Glu Gly His Thr Tyr Val Ala Phe Ile	Arg Met Glu Lys Asp Asp	
575	580	585
Asp Phe Thr Thr Trp Thr Gln Leu Ala	Lys Cys Leu His Ile Trp	
590	595	600
Asp Leu Asp Val Arg Gly Asn His Arg	Gly Leu Trp Arg Leu Phe	
605	610	615
Arg Lys Lys Asn His Phe Leu Val Val	Gly Val Pro Ala Ser Pro	
620	625	630
Tyr Ser Val Lys Lys Pro Pro Ser Val	Thr Pro Ile Phe Leu Glu	
635	640	645
Pro Pro Pro Lys Glu Glu Gly Ala Pro	Gly Ala Pro Glu Gln Thr	
650	655	660

<210> 89
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 89

gatggcaaaa cgtgtgtttg acacg 25

<210> 90
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 90
cctcaaccag gccacgggcc ac 22

<210> 91
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 91
cccaggcaga gatgcagtac aggc 24

<210> 92
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 92
cctccagtag gtggatggat tggctc 26

<210> 93
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 93
ctcacctcat gaggatgagg ccatggtgct attcctcaac atggtag 47

<210> 94
<211> 3037
<212> DNA
<213> Homo sapiens

ctttcttctt agtttagagg ctctgtact ttatccattg atttttaaca 1500
 tggttcccac catgtaagac tgggtgcttta gcatctatgc cacatgcgtt 1550
 gatggaaggt catagcacc actcacttag atgctaaagg tgattctagt 1600
 taatctggga ttagggtcag gaaaatgata gcaagacaca ttgaaagctc 1650
 tctttatact caaaagagat atccattgaa aagggatgtc tagagggatt 1700
 taaacagctc ctttggcacg tgcctctctg aatccagcct gccattccat 1750
 caaatggagc aggagaggtg ggaggagctt ctaaagaggt gactggtatt 1800
 ttgtagcatt ccttgtcaag ttctcctttg cagaatacct gtctccacat 1850
 tcctagagag gagccaagtt ctagtagttt cagttctagg ctttccttca 1900
 agaacagtca gatcaciaaag tgtctttgga aattaaggga tattaattt 1950
 taagtgattt ttggatggtt attgatattt ttgtagtagc tttttttaa 2000
 agactaccaa aatgtatggt tgtccttttt ttttgttttt tttttttta 2050
 attattttct ttagcagatc agcaatccct ctagggacct aaatactagg 2100
 tcagcttttg cgacactgtg tcttctcaca taaccacctg tagcaagatg 2150
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 ctttctatac catttcaaaa cacattacac taagggggaa ccaagactag 2650
 tttcttcagg gcagtggacg tagtagtttg taaaaacgtt ttctatgacg 2700
 cataagctag catgcctatg atttatttcc ttcatgaatt tgtcactgga 2750
 tcagcagctg tggaaataaa gcttgtgagc cctctgctgg ccacagtgag 2800
 gaaagtagca caaataggat acagttgtat gtagtcattg gcaacaattg 2850
 catacaattt tactaccaag agaaggtata gtatggaaag tccaaatgac 2900

ttccttgatt ggatgttaac agctgactgg tgtgagactt gaggtttcat 2950
ctagtccttc aaaactatat ggttgccctag attctctctg gaaactgact 3000
ttgtcaaata aatagcagat tgtagtgtca aaaaaaa 3037

<210> 95
<211> 307
<212> PRT
<213> Homo sapiens

<400> 95
Met Asp Asp Phe Ile Ser Ile Ser Leu Leu Ser Leu Ala Met Leu
1 5 10 15
Val Gly Cys Tyr Val Ala Gly Ile Ile Pro Leu Ala Val Asn Phe
20 25 30
Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu
35 40 45
Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
50 55 60
Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
65 70 75
Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
80 85 90
Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
95 100 105
Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
110 115 120
Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
125 130 135
Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
140 145 150
Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
155 160 165
Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
170 175 180
Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
185 190 195
Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
200 205 210
Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
215 220 225
Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

230	235	240
Asn Ala Thr Gly Val Ala Met Leu Phe	Ser Ala Gly Thr Phe	Leu
245	250	255
Tyr Val Ala Thr Val His Val Leu Pro	Glu Val Gly Gly Ile	Gly
260	265	270
His Ser His Lys Pro Asp Ala Thr Gly	Gly Arg Gly Leu Ser	Arg
275	280	285
Leu Glu Val Ala Ala Leu Val Leu Gly	Cys Leu Ile Pro Leu	Ile
290	295	300
Leu Ser Val Gly His Gln His		
305		

<210> 96
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 96
 gttgtgggtg aataaaggag ggcag 25

<210> 97
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 97
 ctgtgctcat gttcatggac aactg 25

<210> 98
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 98
 ggatgatttc atctccatta gctgctgtc tctggctatg ttggtgggat 50

<210> 99
 <211> 1429

cgaagagatg actataaaat gttcatgagg gactgaatac tgaaaactgt 1400

gaaatgtact aaataaaatg tacatctga 1429

$\langle 210 \rangle$ 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

Met Met Gly Leu Gly Asn Gly Arg Arg Ser Met Lys Ser Pro Pro
1 5 10 15

Leu Val Leu Ala Ala Leu Val Ala Cys Ile Ile Val Leu Gly Phe
20 25 30

Asn Tyr Trp Ile Ala Ser Ser Arg Ser Val Asp Leu Gln Thr Arg
35 40 45

Ile Met Glu Leu Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg
50 55 60

Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu
65 70 75

Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser Ser His Asn Phe
80 85 90

Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val
95 100 105

Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu
110 115 120

Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln
125 130 135

Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg
140 145 150

Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu
155 160 165

Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys
170 175 180

Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp
185 190 195

Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu
200 205 210

Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly
215 220 225

Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser
230 235 240

Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr
 245 250 255
 Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu
 260 265 270
 Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val
 275 280 285
 Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro
 290 295 300
 Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met
 305 310 315
 Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu
 320 325 330
 Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu
 335 340 345
 Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser
 350 355 360
 Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile
 365 370 375
 Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu
 380 385 390
 Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu
 395 400

<210> 101
 <211> 3671
 <212> DNA
 <213> Homo sapiens

<400> 101
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 ggagctcacc aaccatagca gctgccaaga gccccaggc cctgggtccc 150
 tgccatgggg gagccaaggg aaacctgggg cctgctggat ggcttcccga 200
 ttttcgcggg ttgtgttggg gctgatagat gctctgcgat ttgacttcgc 250
 ccagccccag cattcacacg tgcctagaga gcctcctgtc tccctaccct 300
 tcctgggcaa actaagctcc ttgcagagga tcctggagat tcagccccac 350
 catgcccggc tctaccgatc tcaggttgac cctcctacca ccaccatgca 400
 ggcctcaag gccctacca ctggctcact gcctaccttt attgatgctg 450
 gtagtaactt cgccagccac gccatagtgg aagacaatct cattaagcag 500

ctcaccagtg	caggaaggcg	tgtagtcttc	atgggagatg	atacctggaa	550
agaccttttc	cctggtgctt	tctccaaagc	tttcttcttc	ccatccttca	600
atgtcagaga	cctagacaca	gtggacaatg	gcatcctgga	acacctctac	650
cccaccatgg	acagtgggtga	atgggacgtg	ctgattgctc	acttcctggg	700
tgtggaccac	tgtggccaca	agcatggccc	tcaccaccct	gaaatggcca	750
agaaacttag	ccagatggac	caggtgatcc	agggacttgt	ggagcgtctg	800
gagaatgaca	cactgctggt	agtggctggg	gaccatggga	tgaccacaaa	850
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gtgattcctc	aagttagcct	tgtgcccacg	ctggccctgc	tgctgggcct	1000
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tcacaatgcc	ccgccttggc	acttcagcca	caacaaacct	cccacggcac	1850
aatggtgcat	atgccctgag	gcttgaatt	gggttgcttt	tatgtacaag	1900
gctagctggg	cttttctatc	gttgccctga	agagacacct	gtttgccact	1950

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 aatttatggt atggagcttg tgtggcggcg ctggtagctgc 2050
 cgtgcgcttg tggcttcgcc gctatggtaa tctcaagagc cccgagccac 2100
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 acagagagt ctggagaaca gtgtagcctg gcctgtacag gtactggatg 3350
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 cagcactttg ggaggcagag gtgggaggat tgcttggtcc caggagtcca 3600
 agaccagcct gtggaacata acaagacccc gtctctacta tttaaaaaaa 3650
 agtgtaataa aatgataata t 3671

<210> 102
 <211> 1089
 <212> PRT
 <213> Homo sapiens

<400> 102
 Met Gln Lys Ala Ser Val Leu Leu Phe Leu Ala Trp Val Cys Phe
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 Leu Phe Tyr Ala Gly Ile Ala Leu Phe Thr Ser Gly Phe Leu Leu
 20 25 30
 Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro
 35 40 45
 Gly Pro Gly Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala
 50 55 60
 Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile
 65 70 75
 Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val
 80 85 90
 Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser
 95 100 105
 Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu
 110 115 120
 Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu
 125 130 135
 Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly
 140 145 150
 Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys
 155 160 165
 Gln Leu Thr Ser Ala Gly Arg Arg Val Val Phe Met Gly Asp Asp
 170 175 180
 Thr Trp Lys Asp Leu Phe Pro Gly Ala Phe Ser Lys Ala Phe Phe
 185 190 195
 Phe Pro Ser Phe Asn Val Arg Asp Leu Asp Thr Val Asp Asn Gly

200										205					210				
Ile	Leu	Glu	His	Leu	Tyr	Pro	Thr	Met	Asp	Ser	Gly	Glu	Trp	Asp					
				215					220					225					
Val	Leu	Ile	Ala	His	Phe	Leu	Gly	Val	Asp	His	Cys	Gly	His	Lys					
				230					235					240					
His	Gly	Pro	His	His	Pro	Glu	Met	Ala	Lys	Lys	Leu	Ser	Gln	Met					
				245					250					255					
Asp	Gln	Val	Ile	Gln	Gly	Leu	Val	Glu	Arg	Leu	Glu	Asn	Asp	Thr					
				260					265					270					
Leu	Leu	Val	Val	Ala	Gly	Asp	His	Gly	Met	Thr	Thr	Asn	Gly	Asp					
				275					280					285					
His	Gly	Gly	Asp	Ser	Glu	Leu	Glu	Val	Ser	Ala	Ala	Leu	Phe	Leu					
				290					295					300					
Tyr	Ser	Pro	Thr	Ala	Val	Phe	Pro	Ser	Thr	Pro	Pro	Glu	Glu	Pro					
				305					310					315					
Glu	Val	Ile	Pro	Gln	Val	Ser	Leu	Val	Pro	Thr	Leu	Ala	Leu	Leu					
				320					325					330					
Leu	Gly	Leu	Pro	Ile	Pro	Phe	Gly	Asn	Ile	Gly	Glu	Val	Met	Ala					
				335					340					345					
Glu	Leu	Phe	Ser	Gly	Gly	Glu	Asp	Ser	Gln	Pro	His	Ser	Ser	Ala					
				350					355					360					
Leu	Ala	Gln	Ala	Ser	Ala	Leu	His	Leu	Asn	Ala	Gln	Gln	Val	Ser					
				365					370					375					
Arg	Phe	Leu	His	Thr	Tyr	Ser	Ala	Ala	Thr	Gln	Asp	Leu	Gln	Ala					
				380					385					390					
Lys	Glu	Leu	His	Gln	Leu	Gln	Asn	Leu	Phe	Ser	Lys	Ala	Ser	Ala					
				395					400					405					
Asp	Tyr	Gln	Trp	Leu	Leu	Gln	Ser	Pro	Lys	Gly	Ala	Glu	Ala	Thr					
				410					415					420					
Leu	Pro	Thr	Val	Ile	Ala	Glu	Leu	Gln	Gln	Phe	Leu	Arg	Gly	Ala					
				425					430					435					
Arg	Ala	Met	Cys	Ile	Glu	Ser	Trp	Ala	Arg	Phe	Ser	Leu	Val	Arg					
				440					445					450					
Met	Ala	Gly	Gly	Thr	Ala	Leu	Leu	Ala	Ala	Ser	Cys	Phe	Ile	Cys					
				455					460					465					
Leu	Leu	Ala	Ser	Gln	Trp	Ala	Ile	Ser	Pro	Gly	Phe	Pro	Phe	Cys					
				470					475					480					
Pro	Leu	Leu	Leu	Thr	Pro	Val	Ala	Trp	Gly	Leu	Val	Gly	Ala	Ile					
				485					490					495					

Ala Tyr Ala Gly	Leu 500	Leu Gly Thr Ile	Glu 505	Leu Lys Leu Asp	Leu 510
Val Leu Leu Gly	Ala 515	Val Ala Ala Val	Ser 520	Ser Phe Leu Pro	Phe 525
Leu Trp Lys Ala	Trp 530	Ala Gly Trp Gly	Ser 535	Lys Arg Pro Leu	Ala 540
Thr Leu Phe Pro	Ile 545	Pro Gly Pro Val	Leu 550	Leu Leu Leu Leu	Phe 555
Arg Leu Ala Val	Phe 560	Phe Ser Asp Ser	Phe 565	Val Val Ala Glu	Ala 570
Arg Ala Thr Pro	Phe 575	Leu Leu Gly Ser	Phe 580	Ile Leu Leu Leu	Val 585
Val Gln Leu His	Trp 590	Glu Gly Gln Leu	Leu 595	Pro Pro Lys Leu	Leu 600
Thr Met Pro Arg	Leu 605	Gly Thr Ser Ala	Thr 610	Thr Asn Pro Pro	Arg 615
His Asn Gly Ala	Tyr 620	Ala Leu Arg Leu	Gly 625	Ile Gly Leu Leu	Leu 630
Cys Thr Arg Leu	Ala 635	Gly Leu Phe His	Arg 640	Cys Pro Glu Glu	Thr 645
Pro Val Cys His	Ser 650	Ser Pro Trp Leu	Ser 655	Pro Leu Ala Ser	Met 660
Val Gly Gly Arg	Ala 665	Lys Asn Leu Trp	Tyr 670	Gly Ala Cys Val	Ala 675
Ala Leu Val Ala	Leu 680	Leu Ala Ala Val	Arg 685	Leu Trp Leu Arg	Arg 690
Tyr Gly Asn Leu	Lys 695	Ser Pro Glu Pro	Pro 700	Met Leu Phe Val	Arg 705
Trp Gly Leu Pro	Leu 710	Met Ala Leu Gly	Thr 715	Ala Ala Tyr Trp	Ala 720
Leu Ala Ser Gly	Ala 725	Asp Glu Ala Pro	Pro 730	Arg Leu Arg Val	Leu 735
Val Ser Gly Ala	Ser 740	Met Val Leu Pro	Arg 745	Ala Val Ala Gly	Leu 750
Ala Ala Ser Gly	Leu 755	Ala Leu Leu Leu	Trp 760	Lys Pro Val Thr	Val 765
Leu Val Lys Ala	Gly 770	Ala Gly Ala Pro	Arg 775	Thr Arg Thr Val	Leu 780
Thr Pro Phe Ser	Gly	Pro Pro Thr Ser	Gln	Ala Asp Leu Asp	Tyr

785	790	795
Val Val Pro Gln Ile Tyr Arg His Met	Gln Glu Glu Phe Arg Gly	
800	805	810
Arg Leu Glu Arg Thr Lys Ser Gln Gly	Pro Leu Thr Val Ala Ala	
815	820	825
Tyr Gln Leu Gly Ser Val Tyr Ser Ala	Ala Met Val Thr Ala Leu	
830	835	840
Thr Leu Leu Ala Phe Pro Leu Leu Leu	Leu His Ala Glu Arg Ile	
845	850	855
Ser Leu Val Phe Leu Leu Leu Phe Leu	Gln Ser Phe Leu Leu Leu	
860	865	870
His Leu Leu Ala Ala Gly Ile Pro Val	Thr Thr Pro Gly Pro Phe	
875	880	885
Thr Val Pro Trp Gln Ala Val Ser Ala	Trp Ala Leu Met Ala Thr	
890	895	900
Gln Thr Phe Tyr Ser Thr Gly His Gln	Pro Val Phe Pro Ala Ile	
905	910	915
His Trp His Ala Ala Phe Val Gly Phe	Pro Glu Gly His Gly Ser	
920	925	930
Cys Thr Trp Leu Pro Ala Leu Leu Val	Gly Ala Asn Thr Phe Ala	
935	940	945
Ser His Leu Leu Phe Ala Val Gly Cys	Pro Leu Leu Leu Leu Trp	
950	955	960
Pro Phe Leu Cys Glu Ser Gln Gly Leu	Arg Lys Arg Gln Gln Pro	
965	970	975
Pro Gly Asn Glu Ala Asp Ala Arg Val	Arg Pro Glu Glu Glu Glu	
980	985	990
Glu Pro Leu Met Glu Met Arg Leu Arg	Asp Ala Pro Gln His Phe	
995	1000	1005
Tyr Ala Ala Leu Leu Gln Leu Gly Leu	Lys Tyr Leu Phe Ile Leu	
1010	1015	1020
Gly Ile Gln Ile Leu Ala Cys Ala Leu	Ala Ala Ser Ile Leu Arg	
1025	1030	1035
Arg His Leu Met Val Trp Lys Val Phe	Ala Pro Lys Phe Ile Phe	
1040	1045	1050
Glu Ala Val Gly Phe Ile Val Ser Ser	Val Gly Leu Leu Leu Gly	
1055	1060	1065
Ile Ala Leu Val Met Arg Val Asp Gly	Ala Val Ser Ser Trp Phe	
1070	1075	1080

gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg 1300
 agccttctga gggggatggg ctcgagagag agggctcttct atctagactc 1350
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 cgtgtgtgat tgggttcatgc atgtaggtct cttacaatg atgggtgggcc 1650
 tctggagtcc aggggctggc cggttgttct atgcagagaa agcagtcaat 1700
 aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104
 <211> 442
 <212> PRT
 <213> Homo sapiens

<400> 104
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 Leu Leu Thr Leu Cys Ser Ile Ser Ser Gln Ile Gly Pro Pro Glu
 20 25 30
 Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr
 35 40 45
 Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser
 50 55 60
 Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu
 65 70 75
 Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His
 80 85 90
 Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val
 95 100 105
 His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro
 110 115 120
 Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu
 125 130 135
 Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile
 140 145 150
 Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr
 155 160 165

Ile His Val Gly Lys Glu Lys His Pro Ala Asn Leu Ile Leu Ile	170	175	180
Tyr Gly Asn Glu Phe Asp Lys Arg Phe Phe Val Pro Ala Glu Lys	185	190	195
Ile Val Ile Asn Phe Ile Thr Leu Asn Ile Ser Asp Asp Ser Lys	200	205	210
Ile Ser His Gln Asp Met Ser Leu Leu Gly Lys Ser Ser Asp Val	215	220	225
Ser Ser Leu Asn Asp Pro Gln Pro Ser Gly Asn Leu Arg Pro Pro	230	235	240
Gln Glu Glu Glu Glu Val Lys His Leu Gly Tyr Ala Ser His Leu	245	250	255
Met Glu Ile Phe Cys Asp Ser Glu Glu Asn Thr Glu Gly Thr Ser	260	265	270
Leu Thr Gln Gln Glu Ser Leu Ser Arg Thr Ile Pro Pro Asp Lys	275	280	285
Thr Val Ile Glu Tyr Glu Tyr Asp Val Arg Thr Thr Asp Ile Cys	290	295	300
Ala Gly Pro Glu Glu Gln Glu Leu Ser Leu Gln Glu Glu Val Ser	305	310	315
Thr Gln Gly Thr Leu Leu Glu Ser Gln Ala Ala Leu Ala Val Leu	320	325	330
Gly Pro Gln Thr Leu Gln Tyr Ser Tyr Thr Pro Gln Leu Gln Asp	335	340	345
Leu Asp Pro Leu Ala Gln Glu His Thr Asp Ser Glu Glu Gly Pro	350	355	360
Glu Glu Glu Pro Ser Thr Thr Leu Val Asp Trp Asp Pro Gln Thr	365	370	375
Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser	380	385	390
Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly	395	400	405
Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro	410	415	420
Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly	425	430	435
Leu Tyr Val Gln Met Glu Asn	440		

<210> 105

<222> 1-51
<223> Synthetic construct.

<400> 109
ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaaca 50
c 51

<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

<400> 110
cggacgcgtg ggcggacgcg tgggcggacg cgtgggtctc tgcggggaga 50
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tctgctgact gtggccaccg ccctgatgct gcccgtaag cccccgcag 150
gtcctgggg ggcccagatc atcgggggcc acgaggtgac cccccactcc 200
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ctggggcttc gtgtctgact ttgaggagct gccgctgga ctgatggagg 600
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cacctgacac ttaccatgct ctgcaccgc agtggggaca gccacagacg 700
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ggttcggcgg agcagtcacc agcccgccc cctgcctggg accaccaggc 900
ccccaggaga agccgctga gccacaacct tgcggcatgc aatgagatg 950
gccgctccag gcctggaatg ttccgtggct gggcccccac ggaagcctga 1000
tgttcagggg tggggtggga cgggcagcgg tggggcacac ccattccaca 1050
tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
275 280

<210> 112
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 112
gacgtctgca acagctcctg gaag 24

<210> 113
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 113
cgagaaggaa acgaggccgt gag 23

<210> 114
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 114
tgacacttac catgctctgc acccgcagtg gggacagcca caga 44

<210> 115
<211> 1808
<212> DNA
<213> Homo sapiens

<400> 115
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cctgacgcct gacgcctgtc cccggccccg catgagccgc tacctgctgc 100
cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150
tatgtcaccg gtggggcttg ccccagcaag gccaccatcc ctgggaagac 200

ggtcatcgtg acgggcgcca acacagggcat cggaagcag accgccttgg 250
 aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300
 aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350
 tgtcaacgcc cggcacctgg acttggcttc cctcaagtct atccgagagt 400
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 aacgcgggtg tgatgcggtg cccccactgg accaccgagg acggcttcga 500
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 actgtcaacg ccctgcaccc cggcgtggcc aggacagagc tgggcagaca 800
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 ggaggctttg ggctgaaagt gcccgcctgg tgggcttaga ggctccctct 1050
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 ctggcactac ctgagccggg agaccagga ctggcggccg ccatgcccgc 1200
 agtaggttct agggggcggt gctggccgca gtggactggc ctgcaggtga 1250
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 agaggggcca tctgatgctt cccctgggaa tctaaactgg gaatggccga 1350
 ggaggaaggg gctctgtgca cttgcaggcc acgtcaggag agccagcgg 1400
 gcctgtcggg gaggggtcca aggtgctccg tgaagagcat gggcaagttg 1450
 tctgacactt ggtggattct tgggtccctg tgggacctg tgcattgatg 1500
 gtcctctctg agccttggtt tcttcagcag tgagatgctc agaataactg 1550
 ctgtctccca tgatggtgtg gtacagcgag ctgttgctg gctatggcat 1600
 ggctgtgccg ggggtgtttg ctgagggtt cctgtgccag agcccagcca 1650

gagagcaggt gcaggtgtca tcccagattc aggctctgca cggcatggag 1700
 tgggaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750
 caccttcta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800
 gctcattt 1808

<210> 116
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 116
 Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala
 1 5 10 15
 Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys
 20 25 30
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
 50 55 60
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
 65 70 75
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
 80 85 90
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
 95 100 105
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
 110 115 120
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
 125 130 135
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
 140 145 150
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
 155 160 165
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
 170 175 180
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
 185 190 195
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
 200 205 210
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
 215 220 225

tacattatat aaggattttt ttttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118
 <211> 544
 <212> PRT
 <213> Homo sapiens

<400> 118
 Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
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 Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr
 20 25 30
 Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
 35 40 45
 Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
 50 55 60
 Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
 65 70 75
 His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
 80 85 90
 Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
 95 100 105
 Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
 110 115 120
 Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
 125 130 135
 Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
 140 145 150
 Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
 155 160 165
 Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
 170 175 180
 Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
 185 190 195
 Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
 200 205 210
 Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
 215 220 225
 Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
 230 235 240

Gly Asn Val Ser	Cys Ala Leu Ser Leu	Ser Arg Glu Phe Leu Leu	245	250	255
Tyr Ser Pro Asp	Asn Lys Arg Met Ala	Arg Asn Val Leu Lys Tyr	260	265	270
Glu Arg Leu Leu	Ala Glu Ser Pro Asn	His Val Val Ala Glu Ala	275	280	285
Val Ile Gln Arg	Pro Asn Ile Pro His	Leu Gln Thr Arg Asp Thr	290	295	300
Tyr Glu Gly Leu	Cys Gln Thr Leu Gly	Ser Gln Pro Thr Leu Tyr	305	310	315
Gln Ile Pro Ser	Leu Tyr Cys Ser Tyr	Glu Thr Asn Ser Asn Ala	320	325	330
Tyr Leu Leu Leu	Gln Pro Ile Arg Lys	Glu Val Ile His Leu Glu	335	340	345
Pro Tyr Ile Ala	Leu Tyr His Asp Phe	Val Ser Asp Ser Glu Ala	350	355	360
Gln Lys Ile Arg	Glu Leu Ala Glu Pro	Trp Leu Gln Arg Ser Val	365	370	375
Val Ala Ser Gly	Glu Lys Gln Leu Gln	Val Glu Tyr Arg Ile Ser	380	385	390
Lys Ser Ala Trp	Leu Lys Asp Thr Val	Asp Pro Lys Leu Val Thr	395	400	405
Leu Asn His Arg	Ile Ala Ala Leu Thr	Gly Leu Asp Val Arg Pro	410	415	420
Pro Tyr Ala Glu	Tyr Leu Gln Val Val	Asn Tyr Gly Ile Gly Gly	425	430	435
His Tyr Glu Pro	His Phe Asp His Ala	Thr Ser Pro Ser Ser Pro	440	445	450
Leu Tyr Arg Met	Lys Ser Gly Asn Arg	Val Ala Thr Phe Met Ile	455	460	465
Tyr Leu Ser Ser	Val Glu Ala Gly Gly	Ala Thr Ala Phe Ile Tyr	470	475	480
Ala Asn Leu Ser	Val Pro Val Val Arg	Asn Ala Ala Leu Phe Trp	485	490	495
Trp Asn Leu His	Arg Ser Gly Glu Gly	Asp Ser Asp Thr Leu His	500	505	510
Ala Gly Cys Pro	Val Leu Val Gly Asp	Lys Trp Val Ala Asn Lys	515	520	525
Trp Ile His Glu	Tyr Gly Gln Glu Phe	Arg Arg Pro Cys Ser Ser			

530

535

540

Ser Pro Glu Asp

<210> 119
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 119
cgggacagga gacccagaaa ggg 23

<210> 120
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 120
ggccaagtga tccaaggcat cttc 24

<210> 121
<211> 49
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-49
<223> Synthetic construct.

<400> 121
ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122
<211> 1778
<212> DNA
<213> Homo sapiens

<400> 122
gagataggga gtctgggttt aagttcctgc tccatctcag gagcccctgc 50
tcccaccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100
gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150
ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250
gctcaagttt tcacttatca tctattccac cgtgttctgg ctgattgggg 300
ccctggtcct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350
aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcacccctct 400
gggcgtcgtc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450
gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500
ctcatcatgg agctcattgg tggcgtgggtg gccttgacct tccggaacca 550
gaccattgac ttctgaacg acaacattcg aagaggaatt gagaactact 600
atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650
aagtgtgtg gcggggagga ctaccgagat tggagcaaga atcagtacca 700
cgactgcagt gccctggac cctggcctg tggggtgccc tacacctgct 750
gcatcaggaa cagcacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800
atcgacaagg agcgtttcag tgtgcaggat gtcactacg tgcggggctg 850
caccaacgcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900
gcatcctcct gggcatcctg cttccccagt tctgggggt gctgctgacg 950
ctgctgtaca tcaccgggt ggaggacatc atcatggagc actctgtcac 1000
tgatgggctc ctggggcccg gtgccaagcc cagcgtggag gcggcaggca 1050
cgggatgctg cttgtgctac cccaattagg gccagcctg ccatggcagc 1100
tccaacaagg accgtctggg atagcacctc tcagtcaaca tcgtggggct 1150
ggacagggt gcggcccctc tgcccacact cagtactgac caaagccagg 1200
gctgtgtgtg cctgtgtgta ggtcccacgg cctctgcctc ccaggaggc 1250
agagcctggg cctcccctaa gaggctttcc ccgaggcagc tctggaatct 1300
gtgccacct ggggcctggg gaacaaggcc ctcccttctc caggcctggg 1350
ctacagggga gggagagcct gaggtctgctc tcagggccca tttcatctct 1400
ggcagtgcct tggcgggtgt attcaaggca gttttgtagc acctgtaatt 1450
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gggcaggagg gaagagctgt ccatgcagcc acgcccattg ccaggttggc 1550
ctcttctcag cctcccaggt gccttgagcc ctcttgcaag ggcggctgct 1600
tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700
gtcttattct tgcccttccc ccaaccagtt tgtaatacaa acaataaaaaa 1750
catgttttgt tttgttttta aaaaaaaa 1778

<210> 123
<211> 294
<212> PRT
<213> Homo sapiens

<400> 123

Met	Pro	Arg	Gly	Asp	Ser	Glu	Gln	Val	Arg	Tyr	Cys	Ala	Arg	Phe	1	5	10	15
Ser	Tyr	Leu	Trp	Leu	Lys	Phe	Ser	Leu	Ile	Ile	Tyr	Ser	Thr	Val	20	25	30	
Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala	35	40	45	
Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu	50	55	60	
Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met	65	70	75	
Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr	80	85	90	
Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met	95	100	105	
Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr	110	115	120	
Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr	125	130	135	
Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys	140	145	150	
Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys	155	160	165	
Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly	170	175	180	
Val	Pro	Tyr	Thr	Cys	Cys	Ile	Arg	Asn	Thr	Thr	Glu	Val	Val	Asn	185	190	195	
Thr	Met	Cys	Gly	Tyr	Lys	Thr	Ile	Asp	Lys	Glu	Arg	Phe	Ser	Val	200	205	210	
Gln	Asp	Val	Ile	Tyr	Val	Arg	Gly	Cys	Thr	Asn	Ala	Val	Ile	Ile	215	220	225	
Trp	Phe	Met	Asp	Asn	Tyr	Thr	Ile	Met	Ala	Cys	Ile	Leu	Leu	Gly				

230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu Tyr	
245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp	
260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala Gly	
275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn		
290		

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 124
 atcatctatt ccaccgtgtt ctggc 25

<210> 125
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 125
 gacagagtgc tccatgatga tgtcc 25

<210> 126
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 126
 cctgtctgtg ggcattctatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127
 <211> 1636
 <212> DNA
 <213> Homo sapiens

<400> 127

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcactt 50
 gctgccctct gacacctggg aagatggccg gcccgaggac cttcaccctt 100
 ctctgtggtt tgctggcagc caccttgatc caagccacc ctagtcccac 150
 tgcagttctc atcctcgcc caaaagtcac caaagaaaag ctgacacagg 200
 agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250
 agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300
 ggtgaacacc gtctgaagc acatcatctg gctgaaggct atcacagcta 350
 acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta 400
 gtcaagatcc ccttgacat ggtggctgga ttcaacacgc ccttggtcaa 450
 gaccatcgtg gagttccaca tgacgactga ggccaagcc accatccgca 500
 tggacaccag tgcaagtggc cccaccgcc tggctcctcag tgactgtgcc 550
 accagccatg ggagcctgcg catccaactg ctgtataagc tctccttcct 600
 ggtgaacgcc ttagctaagc aggtcatgaa cctcctagt ccatccctgc 650
 ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat 700
 ggcattgtatg cagacctcct gcagctggtg aaggtgccc tttccctcag 750
 cattgaccgt ctggagtttg accttctgta tcctgccatc aagggtgaca 800
 ccattcagct ctacctgggg gccaaagttgt tggactcaca gggaaagggtg 850
 accaagtgggt tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900
 caacatcccg ttcagcctca tcgtgagtca ggacgtggtg aaagctgcag 950
 tggctgctgt gctctctcca gaagaattca tggctcctgtt ggactctgtg 1000
 cttcctgaga gtgcccacgc gctgaagtca agcatcgggc tgatcaatga 1050
 aaaggctgca gataagctgg gatctacca gatcgtgaag atcctaactc 1100
 aggacactcc cgagtttttt atagaccaag gccatgccaa ggtggcccaa 1150
 ctgatcgtgc tggaagtgtt tccctccagt gaagccctcc gccctttgtt 1200
 caccctgggc atcgaagcca gctcggaagc tcagttttac accaaagggtg 1250
 accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300
 atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350
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 gatctgggggt ccagtggtca ttggtgaagg ccttggggatt cgaggcagct 1450

gagtcctcac tgaccaagga tgcccttggtg cttactccag cctccttggtg 1500
 gaaacccagc tctcctgtct cccagtgaag acttggtatgg cagccatcag 1550
 ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600
 cctctctgca atcaataaac acttgccctgt gaaaaa 1636

<210> 128
 <211> 484
 <212> PRT
 <213> Homo sapiens

<400> 128
 Met Ala Gly Pro Trp Thr Phe Thr Leu Leu Cys Gly Leu Leu Ala
 1 5 10 15
 Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile
 20 25 30
 Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys
 35 40 45
 Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser
 50 55 60
 Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser
 65 70 75
 Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile
 80 85 90
 Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp
 95 100 105
 Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe
 110 115 120
 Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr
 125 130 135
 Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro
 140 145 150
 Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu
 155 160 165
 Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu
 170 175 180
 Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu
 185 190 195
 Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly
 200 205 210
 Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu
 215 220 225

Ser Ile Asp Arg	Leu Glu Phe Asp Leu	Leu Tyr Pro Ala Ile Lys
230	235	240
Gly Asp Thr Ile	Gln Leu Tyr Leu Gly	Ala Lys Leu Leu Asp Ser
245	250	255
Gln Gly Lys Val	Thr Lys Trp Phe Asn	Asn Ser Ala Ala Ser Leu
260	265	270
Thr Met Pro Thr	Leu Asp Asn Ile Pro	Phe Ser Leu Ile Val Ser
275	280	285
Gln Asp Val Val	Lys Ala Ala Val Ala	Ala Val Leu Ser Pro Glu
290	295	300
Glu Phe Met Val	Leu Leu Asp Ser Val	Leu Pro Glu Ser Ala His
305	310	315
Arg Leu Lys Ser	Ser Ile Gly Leu Ile	Asn Glu Lys Ala Ala Asp
320	325	330
Lys Leu Gly Ser	Thr Gln Ile Val Lys	Ile Leu Thr Gln Asp Thr
335	340	345
Pro Glu Phe Phe	Ile Asp Gln Gly His	Ala Lys Val Ala Gln Leu
350	355	360
Ile Val Leu Glu	Val Phe Pro Ser Ser	Glu Ala Leu Arg Pro Leu
365	370	375
Phe Thr Leu Gly	Ile Glu Ala Ser Ser	Glu Ala Gln Phe Tyr Thr
380	385	390
Lys Gly Asp Gln	Leu Ile Leu Asn Leu	Asn Asn Ile Ser Ser Asp
395	400	405
Arg Ile Gln Leu	Met Asn Ser Gly Ile	Gly Trp Phe Gln Pro Asp
410	415	420
Val Leu Lys Asn	Ile Ile Thr Glu Ile	Ile His Ser Ile Leu Leu
425	430	435
Pro Asn Gln Asn	Gly Lys Leu Arg Ser	Gly Val Pro Val Ser Leu
440	445	450
Val Lys Ala Leu	Gly Phe Glu Ala Ala	Glu Ser Ser Leu Thr Lys
455	460	465
Asp Ala Leu Val	Leu Thr Pro Ala Ser	Leu Trp Lys Pro Ser Ser
470	475	480

Pro Val Ser Gln

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

<400> 129

gagcgaacat ggcagcgcgt tggcgggtttt ggtgtgtctc tgtgaccatg 50
 gtggtggcgc tgctcatcgt ttgcgacggt ccctcagcct ctgccccaaag 100
 aaagaaggag atggtgttat ctgaaaagggt tagtcagctg atggaatgga 150
 ctaacaaaag acctgtaata agaataaatg gagacaagtt ccgtcgcctt 200
 gtgaaagccc caccgagaaa ttactccggt atcgtcatgt tcaactgctct 250
 ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300
 agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350
 ttttttgcca tgggtggattt tgatgaaggc tctgatgtat ttcagatgct 400
 aaacatgaat tcagctccaa ctttcatcaa ctttctgca aaagggaac 450
 ccaaacgggg tgatacatat gagttacagg tgcgggggtt ttcagctgag 500
 cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550
 tagacccccca aattatgctg gtcccttat gttgggattg cttttggctg 600
 ttattggtgg acttgtgtat cttcgaagaa gtaatatgga atttctcttt 650
 aataaaactg gatgggcttt tgcagctttg tgttttgtgc ttgctatgac 700
 atctggtcaa atgtggaacc atataagagg accaccatat gcccataaga 750
 atccccacac gggacatgtg aattatatcc atggaagcag tcaagcccag 800
 tttgtagctg aaacacacat tgttctcttg tttaatggtg gagttacctt 850
 aggaatggtg cttttatgtg aagctgctac ctctgacatg gatattggaa 900
 agcgaaagat aatgtgtgtg gctgggtattg gacttgttgt attattcttc 950
 agttggatgc tctctatttt tagatctaaa tatcatggct acccatacag 1000
 ctttctgatg agttaaaaag gtcccagaga tatatagaca ctggagtact 1050
 ggaaattgaa aaacgaaaat cgtgtgtgtt tgaaaagaag aatgcaactt 1100
 gtatattttg tattacctct ttttttcaag tgatttaaat agttaatcat 1150
 ttaaccaaag aagatgtgta gtgccttaac aagcaatcct ctgtcaaaat 1200
 ctgaggtatt tgaaaataat taccctctta accttctctt cccagtgaac 1250
 tttatggaac atttaattta gtacaattaa gtatattata aaaattgtaa 1300
 aactactact ttgttttagt tagaaciaag ctcaaaacta ctttagtta 1350
 cttggtcatc tgattttata ttgccttacc caaagatggg gaaagtaagt 1400
 cctgaccagg tgttcccaca tatgctgtt acagataact acattaggaa 1450

ttcattctta gcttcttcat ctttgtgtgg atgtgtatac tttacgcac 1500
 tttccttttg agtagagaaa ttatgtgtgt catgtggtct tctgaaaatg 1550
 gaacaccatt cttcagagca cacgtctagc cctcagcaag acagttgttt 1600
 ctctcctcc ttgcatattt cctactgcgc tccagcctga gtgatagagt 1650
 gagactctgt ctcaaaaaaa agtatctcta aatacaggat tataatttct 1700
 gcttgagtat ggtgttaact accttgtatt tagaaagatt tcagattcat 1750
 tccatctcct tagttttctt ttaaggtgac ccatctgtga taaaaatata 1800
 gcttagtgct aaaatcagtg taacttatac atggcctaaa atgtttctac 1850
 aaattagagt ttgtcactta ttccatttgt acctagaga aaaataggct 1900
 cagttagaaa aggactccct ggccaggcgc agtgacttac gcctgtaatc 1950
 tcagcacttt gggaggccaa ggcaggcaga tcacgaggtc aggagttcga 2000
 gaccatcctg gccaacatgg tgaaaccccg tctctactaa aaatataaaa 2050
 attagctggg tgtggtggca ggagcctgta atcccagcta cacaggaggc 2100
 tgaggcacga gaatcacttg aactcaggag atggagggtt cagtgagccg 2150
 agatcacgcc actgcactcc agcctggcaa cagagcgaga ctccatctca 2200
 aaaaaaaaaaaa aaa 2213

<210> 130
 <211> 335
 <212> PRT
 <213> Homo sapiens

<400> 130
 Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val
 1 5 10 15
 Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln
 20 25 30
 Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met
 35 40 45
 Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
 50 55 60
 Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
 65 70 75
 Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
 80 85 90
 Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
 95 100 105

tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150
cttggcgctg gcggtactgg cccccggagc aggggagcag agggcgagag 200
cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250
aggttaacat ttcattccagg aagtcaggta gtgaaacttc cttttatcaa 300
ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350
caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
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<210> 132
 <211> 536
 <212> PRT
 <213> Homo sapiens

<400> 132
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 Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys
 20 25 30
 Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
 35 40 45
 Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
 50 55 60
 Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
 65 70 75

Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys	
				260					265					270	
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu	
				275					280					285	
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu	
				290					295					300	
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly	
				305					310					315	
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr	
				320					325					330	
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile	
				335					340					345	
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile	
				350					355					360	
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn	

365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys		
380	385	390
Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser		
395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg		
410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile		
425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr		
440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln		
455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val		
470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile		
485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln		
500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln		
515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg Ala Val		
530	535	

<210> 133
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 133
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 gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150
 ctacatccta ggccttctgg ggcttttggg cacactgggt gccatgctgc 200
 tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250
 gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300
 catcaccagc tgtgacatct atagcaccct tctgggcctg cccgctgaca 350
 tccaggctgc ccaggccatg atggtgacat ccagtgaat ctctccctg 400
 gcctgcatta tctctgtggg gggcatgaga tgcacagtct tctgccagga 450

atccccgagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500
 ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggatc 550
 ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600
 tggagaggct ctttacttgg gcattatttc ttccctgttc tccctgatag 650
 ctggaatcat cctctgcttt tctgtctcat ccagagaaa tcgctccaac 700
 tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750
 gcctggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800
 cagggtatgt gtgaagaacc agggggccaga gctgggggggt ggctgggtct 850
 gtgaaaaaca gtggacagca ccccgagggc cacagggtgag ggacactacc 900
 actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950
 ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000
 attgccaagg atgctcgcca tgccagcctt tctgttttcc tcaccttgct 1050
 gctccccctgc cctaagtccc caacctcaa cttgaaaccc cattccctta 1100
 agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat 1150
 ccccaaacc actaatcaca tcccactgac tgaccctctg tgatcaaaga 1200
 ccctctctct ggctgagggt ggctcttagc tcattgctgg ggatgggaag 1250
 gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300
 cctccaaaga aactgattgg ccctggaacc tccatccac tcttgttatg 1350
 actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400
 tacggtatcc agggaacaga aagcaggatg caggatggga ggacaggaag 1450
 gcagcctggg acatttaaaa aaata 1475

<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

<400> 134

Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
 1 5 10 15

Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp
 20 25 30

Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
 35 40 45

Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly


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atctcccatc tccagtaaat gtgaaagcag aagacgtttt ccctgagaag 400
acatagaaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
atgacagtag attatcagga aataaataaa gtgggttttc caatgtacac 600
acctgtaaaa 610
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<210> 136
<211> 119
<212> PRT
<213> Homo sapiens
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<400> 136
Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
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Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
          20           25          30

Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
          35           40          45

Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
          50           55          60

Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
          65           70          75

Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
          80           85          90

Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
          95          100         105

Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
          110         115

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<210> 137
<211> 771
<212> DNA
<213> Homo sapiens
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agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150
gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200
gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250
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ctgctttgag cagtgtgtgcc cctggacctt catggtgaag ctgataaacc 300
agaactgcga ctacagcccg acctcggatg acaggctttg tcgcagtgtc 350
agctaattgga acatcagggg aacgatgact cctggattct ccttcctggg 400
tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450
gctgttttggg ggccagagaa acacacactc aactgccac ttcattctgt 500
gacctgtctg aggccacccc tgcagctgcc ctgaggaggc ccacaggtcc 550
cctttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600
ggactctgaa cctcctgat gacccctatg gccaacatca acccggcacc 650
acccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700
atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750
tatgtacttt ataatgaaa a 771

<210> 138
<211> 110
<212> PRT
<213> Homo sapiens.

<400> 138
Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys
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Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met
20 25 30
Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp
35 40 45
Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val
50 55 60
Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg
65 70 75
Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu
80 85 90
Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu
95 100 105
Cys Arg Ser Val Ser
110

<210> 139
<211> 2044
<212> DNA
<213> Homo sapiens

<400> 139

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 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450

140	145	150
Ile Arg His His His Ser Glu His Arg	Val His Gly Ala Met	Glu
155	160	165
Leu Gln Val Gln Thr Gly Lys Asp Ala	Pro Ser Asn Cys Val	Val
170	175	180
Tyr Pro Ser Ser Ser Gln Asp Ser Glu	Asn Ile Thr Ala Ala	Ala
185	190	195
Leu Ala Thr Gly Ala Cys Ile Val Gly	Ile Leu Cys Leu Pro	Leu
200	205	210
Ile Leu Leu Leu Val Tyr Lys Gln Arg	Gln Ala Ala Ser Asn	Arg
215	220	225
Arg Ala Gln Glu Leu Val Arg Met Asp	Ser Asn Ile Gln Gly	Ile
230	235	240
Glu Asn Pro Gly Phe Glu Ala Ser Pro	Pro Ala Gln Gly Ile	Pro
245	250	255
Glu Ala Lys Val Arg His Pro Leu Ser	Tyr Val Ala Gln Arg	Gln
260	265	270
Pro Ser Glu Ser Gly Arg His Leu Leu	Ser Glu Pro Ser Thr	Pro
275	280	285
Leu Ser Pro Pro Gly Pro Gly Asp Val	Phe Phe Pro Ser Leu	Asp
290	295	300
Pro Val Pro Asp Ser Pro Asn Phe Glu	Val Ile	
305	310	

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 cttagacctc ctttctgccc ctcttttctt gccaccgct gtttctggc 150
 ccttctccga ccccgctcta gcagcagacc tcctggggtc tgtgggttga 200
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgact 250
 ccgctcccg accagcggcc tgaccctggg gaaaggatgg ttcccagggt 300
 gagggtctc tctccttgcc tgggactcgc gctgctctgg ttccccctgg 350
 actcccacgc tcgagcccgc ccagacatgt tctgcctttt ccatgggaag 400
 agatactccc ccggcgagag ctggcacccc tacttgagc cacaaggcct 450

gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt 500
accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550
cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600
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agatcttcag tgcccatgag ctgttcccct cccgcctgcc caaccagtgt 700
gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750
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aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850
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tgggagaaaag agaggcccg gcacccagc cccactggc ctcagcgccc 950
ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000
actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050
cggaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100
tcggccctt gccctgcatc ctatgcacct gtgaggatgg ccgccaggac 1150
tgccagcgtg tgacctgtcc caccgagtac ccctgccgtc accccgagaa 1200
agtggctggg aagtgtgca agatttgccc agaggacaaa gcagaccctg 1250
gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
ctcgtccaca catcggtatc cccaagcca gacaacctgc gtcgctttgc 1350
cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg 1400
taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450
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aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550
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ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650
gatatgagct gtataattgt tggtattata tattaataaa taagaagttg 1700
cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142
<211> 451
<212> PRT
<213> Homo sapiens
<400> 142

Met Val Pro Glu Val Arg Val Leu Ser Ser Leu Leu Gly Leu Ala
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Leu Leu Trp Phe Pro Leu Asp Ser His Ala Arg Ala Arg Pro Asp
20 25 30

Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser
35 40 45

Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg
50 55 60

Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His
65 70 75

Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln
80 85 90

Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg
95 100 105

Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His
110 115 120

Gly Glu Ile Phe Ser Ala His Glu Leu Phe Pro Ser Arg Leu Pro
125 130 135

Asn Gln Cys Val Leu Cys Ser Cys Thr Glu Gly Gln Ile Tyr Cys
140 145 150

Gly Leu Thr Thr Cys Pro Glu Pro Gly Cys Pro Ala Pro Leu Pro
155 160 165

Leu Pro Asp Ser Cys Cys Gln Ala Cys Lys Asp Glu Ala Ser Glu
170 175 180

Gln Ser Asp Glu Glu Asp Ser Val Gln Ser Leu His Gly Val Arg
185 190 195

His Pro Gln Asp Pro Cys Ser Ser Asp Ala Gly Arg Lys Arg Gly
200 205 210

Pro Gly Thr Pro Ala Pro Thr Gly Leu Ser Ala Pro Leu Ser Phe
215 220 225

Ile Pro Arg His Phe Arg Pro Lys Gly Ala Gly Ser Thr Thr Val
230 235 240

Lys Ile Val Leu Lys Glu Lys His Lys Lys Ala Cys Val His Gly
245 250 255

Gly Lys Thr Tyr Ser His Gly Glu Val Trp His Pro Ala Phe Arg
260 265 270

Ala Phe Gly Pro Leu Pro Cys Ile Leu Cys Thr Cys Glu Asp Gly
275 280 285

Arg Gln Asp Cys Gln Arg Val Thr Cys Pro Thr Glu Tyr Pro Cys

				290					295					300	
Arg	His	Pro	Glu	Lys 305	Val	Ala	Gly	Lys	Cys 310	Cys	Lys	Ile	Cys	Pro 315	
Glu	Asp	Lys	Ala	Asp 320	Pro	Gly	His	Ser	Glu 325	Ile	Ser	Ser	Thr	Arg 330	
Cys	Pro	Lys	Ala	Pro 335	Gly	Arg	Val	Leu	Val 340	His	Thr	Ser	Val	Ser 345	
Pro	Ser	Pro	Asp	Asn 350	Leu	Arg	Arg	Phe	Ala 355	Leu	Glu	His	Glu	Ala 360	
Ser	Asp	Leu	Val	Glu 365	Ile	Tyr	Leu	Trp	Lys 370	Leu	Val	Lys	Asp	Glu 375	
Glu	Thr	Glu	Ala	Gln 380	Arg	Gly	Glu	Val	Pro 385	Gly	Pro	Arg	Pro	His 390	
Ser	Gln	Asn	Leu	Pro 395	Leu	Asp	Ser	Asp	Gln 400	Glu	Ser	Gln	Glu	Ala 405	
Arg	Leu	Pro	Glu	Arg 410	Gly	Thr	Ala	Leu	Pro 415	Thr	Ala	Arg	Trp	Pro 420	
Pro	Arg	Arg	Ser	Leu 425	Glu	Arg	Leu	Pro	Ser 430	Pro	Asp	Pro	Gly	Ala 435	
Glu	Gly	His	Gly	Gln 440	Ser	Arg	Gln	Ser	Asp 445	Gln	Asp	Ile	Thr	Lys 450	

Thr

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<210> 143
<211> 693
<212> DNA
<213> Homo sapiens
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gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300
cgcaggagaa cgtggccttg aggaagaact ggatggttgg cggcgaaggc 350
ggcgccagcg ggaggtcacc gtgagaccgg acttgcttcc gtgggcgccg 400
gaccttggct tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450
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ccagcggaga gtccggaccg agataccatg ccaggactct ccgggggtcct 500
 gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550
 ttttaaggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
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 20 25 30
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
 35 40 45
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
 50 55 60
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
 65 70 75
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
 80 85 90
 Arg Ser Pro

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
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 caggctgcca tggggcccag caccctctc ctcactttgt tccttttgtc 150
 atggtcggga cccctccaag gacagcagca ccaccttgtg gagtacatgg 200
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350
 acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

gagaccaga accagctct gccctgtgta gagtttgatg agaaggtgac 450
 tggaggccct gggaccaaag gcaagggaag aaggaatgag aagtacgata 500
 tgggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550
 ctgaagcgat ttggtggccc agctggtcta tggaccaagg atccactggg 600
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 aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300
 gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350
 catctttctc actcccatc atttatatta tatccccact aaatttcttg 1400
 ttctcattc ttcaaagtgt ggccagttgt ggctcaaac ctctatattt 1450
 ttagccaatg gcaatcaaat tctttcagct ctttgtttc atacggaact 1500
 ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550
 ttccctcctg ctctcctgcc ccatgtcaac aaatttcagg ctaaggatgc 1600
 ccagaccca gggctctaac cttgtatgcg ggcaggccca gggagcaggc 1650
 agcagtgttc ttcccctcag agtgacttgg ggaggagaa ataggaggag 1700
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 aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800
 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala
				260					265					270
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala
				275					280					285
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys
				290					295					300
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro
				305					310					315
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr
				320					325					330
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile
				335					340					345
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala
				350					355					360
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu
				365					370					375
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly
				380					385					390
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu
				395					400					405

Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
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 gttctcctct tctctctaata ccatccgtca cctctcctgt catccgtttc 150
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
 ttgggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250
 gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300
 gtttcctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350
 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
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ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550
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 tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650
 tcgggctggt tccccggcc cacagcgaag tggaaaggct cacaaggaca 700
 ggatttgtcc acagactcca ggacaaacag agacatgcat ggctgtttg 750
 atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800
 tccatgcggc atgctcatct gagccgagag gtggaatcca gggtagagat 850
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 ttcttctcca aattccagtg gaaaatccag gcggaactgg actggagaag 1000
 aaagcacgga caggcagaat tgagagacgc ccggaacac gcagtggagg 1050
 tgactctgga tccagagacg gctcaccoga agctctgcgt ttctgatctg 1100
 aaaactgtaa cccatagaaa agtccccag gaggtgcctc actctgagaa 1150
 gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcaggga 1200
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 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg 1650
 caaccacgcc ctctctcccc aggggtgaaa tgtaggatga atcacatccc 1700
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aa 2052

<210> 148
<211> 500
<212> PRT
<213> Homo sapiens

<400> 148
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20 25 30
Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys
35 40 45
Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe
50 55 60
Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe
65 70 75
Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp
80 85 90
Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr
95 100 105
Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser
110 115 120
Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly
125 130 135
Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile
140 145 150
Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala
155 160 165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg
170 175 180
Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu
185 190 195
Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His
200 205 210
Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp
215 220 225
Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu

230	235	240
Gly Ile Leu Cys Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu Lys	
245	250	255
Ile Phe Phe Ser Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp	
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys	
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys	
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val	
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val	
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr	
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr	
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg	
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn	
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu	
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu	
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu	
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149

<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgctgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgcca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
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ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150
gcctcgccct gttgtgctgc gccgcgcgcg ccgcgcgcgt cgcctcagcc 200
gcctcggcgg ggaatgtcac cgggtggcggc ggggcccgcg ggcaggtgga 250
cgcgtcgcgc ggccccgggt tgcggggcga gccagccac cccttccta 300
gggcgacggc tcccacggcc caggccccga ggaccgggccc cccgcgcgcc 350
accgtccacc gaccocctggc tgcgaattct ccagcccagt ccccgagac 400

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acctctcagg	cgccgaccag	acccgcgcgg	accacccttt	cgacgaccac	550
tggcccggcg	ccgaccaccc	ctgtagcgac	caccgtaccg	gcgcccacga	600
ctccccggac	cccgaccccc	gatctcccca	gcagcagcaa	cagcagcgtc	650
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tgtagtgaac	tgctctgtgg	ttggaagcct	gaatgtgaat	cgctgcaacc	750
agaccacagg	gcagtgtgag	tgtcggccag	gttatcaggg	gcttcactgt	800
gaaacctgca	aagagggtt	ttacctaaat	tacacttctg	ggctctgtca	850
gccatgtgac	tgtagtccac	atggagctct	cagcataccg	tgcaacaggt	900
aagcaacaga	gggtggaact	gaagttttatt	ttattttagc	aagggaaaaa	950
aaaaggctgc	tactctcaag	gaccatactg	gttttaacaa	aggaggatga	1000
gggtcataga	tttacaaaat	attttatata	cttttattct	cttactttat	1050
atgttatatt	taatgtcagg	atttaaaaac	atctaattta	ctgatttagt	1100
tcttcaaaag	cactagagtc	gccaatTTTT	ctctgggata	atttctgtaa	1150
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tgttttaaga	acttttagct	ccttgacaaa	gaagtgcctt	atacttttagc	1900
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ctactaaaaa	tacaaacaaa	ttagctgggc	gtggtggcac	acacctgtag	2150
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<210> 153
<211> 258
<212> PRT
<213> Homo sapiens
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<400>	153													
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Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn
				20					25					30
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
				35					40					45
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
				50					55					60
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
				65					70					75
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
				80					85					90
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
				95					100					105
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
				110					115					120
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
				125					130					135
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
				140					145					150
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
				155					160					165
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro

<210> 157
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 157
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 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150
 ccgggaaaag ggctttgccca tggagaagga catgaagaac gtcgtggggg 200
 tgggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
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 tgctggccac caacttcaga gactatgccca tcattttcac tcagctggag 400
 ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
 agccagccag gagggcatgg ggctcttcac caagtggagc aggagcctgg 500
 gcttctctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgcccaca 600
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 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 158
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
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 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90

ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000
 gcagagctca gaacctctc ggctctcagc aggtctacct gaacgtctcc 1050
 ctgcagagca aagccacatc aggagtgact caggggggtgg tcgggggagc 1100
 tggagccaca gccctggtct tcctgtcctt ctgcgtcatc ttcgttgtag 1150
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 cttctgcccg ctctcagtg ggggaaggag agctccagta tgcattccctc 1350
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 caccgagtag tcggagatca agatccacag atgagaaact gcagagactc 1450
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 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataaact 1550
 atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600
 tcaaacctga atccacactg tgccctccct tttatttttt taactaaaag 1650
 acagacaaat tccta 1665

<210> 160
 <211> 463
 <212> PRT
 <213> Homo sapiens

<400> 160
 Met Leu Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Ala
 1 5 10 15
 Glu Gly Gln Thr Ser Lys Leu Leu Thr Met Gln Ser Ser Val Thr
 20 25 30
 Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr
 35 40 45
 Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr
 50 55 60
 Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala
 65 70 75
 Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg Asp Arg
 80 85 90
 Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys Thr Leu Ser
 95 100 105
 Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg

110	115	120
Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu		
125	130	135
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile		
140	145	150
Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser		
155	160	165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp		
170	175	180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser		
185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser		
200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn		
215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr		
230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly		
245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu		
260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu		
275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser		
290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala		
305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln		
320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val		
335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe		
350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys		
365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu		
380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr		
395	400	405

Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala
 410 415 420
 Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser
 425 430 435
 Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu
 440 445 450
 Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg
 455 460

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
 gacgcccagt gacctgccga ggctggcagc acagagctct ggagatgaag 50
 accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatgggtg 150
 tcgataagga ctttcgggag gacaggaggc ccaggaaggt gtccccagt 200
 aaggtgacag ccctgggcggt tgggaagttg gaagccacgt tcaccttcac 250
 gagggaggat cggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
 gagctgcccc ggagggacca ctacatcttt tactgcaaag accagcacca 400
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
 accgggaggc cctggaagaa tttaagaaat tgggtgcagc caagggactc 500
 tcggaggagg acattttcac gcccctgcag acgggaagct gcgttcccga 550
 aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctaccc tccagccatg acccttcctt 650
 gctcccaccc acctgactcc aaataaagtc cttttccccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20	25	30
Val Lys Ala Met	Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg	
35	40	45
Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly		
50	55	60
Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile		
65	70	75
Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr		
80	85	90
Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro		
95	100	105
Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly		
110	115	120
Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr		
125	130	135
Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys		
140	145	150
Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser		
155	160	165
Cys Val Pro Glu His		
170		

<210> 163
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 163
 ggagatgaag accctgttcc tg 22

<210> 164
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 164
 ggagatgaag accctgttcc tgggtg 26

<210> 165
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-21
 <223> Synthetic construct.

<400> 165
 gtcctccgga aagtccttat c 21

<210> 166
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 166
 gcctagtgtt cgggaacgca gcttc 25

<210> 167
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 167
 cagggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 168
 ctgtccttca ccctggagga ggaggatatc acagggacct ggtac 45

<210> 169
 <211> 1204
 <212> DNA
 <213> Homo sapiens

<400> 169

gttcgcgaga	tgcagaggtt	gaggtggctg	cgggactgga	agtcatcggg	50
cagaggtctc	acagcagcca	aggaacctg	ggcccgtcc	tccccctcc	100
aggccatgag	gattctgcag	ttaatcctgc	ttgctctggc	aacagggctt	150
gtagggggag	agaccaggat	catcaagggg	ttcgagtgc	agcctcactc	200
ccagccctgg	caggcagccc	tgttcgagaa	gacgcggcta	ctctgtgggg	250
cgacgctcat	cgccccaga	tggctcctga	cagcagccca	ctgcctcaag	300
ccccgctaca	tagttcacct	ggggcagcac	aacctccaga	aggaggagg	350
ctgtgagcag	acccggacag	ccactgagtc	cttccccac	cccggcttca	400
acaacagcct	ccccaacaaa	gaccaccga	atgacatcat	gctggtgaag	450
atggcatcgc	cagtctccat	cacctgggct	gtgcgacccc	tcacctctc	500
ctcacgctgt	gtcactgctg	gcaccagctg	cctcatttcc	ggctggggca	550
gcacgtccag	ccccagtta	cgctgcctc	acaccttgcg	atgcgccaac	600
atcaccatca	ttgagcacca	gaagtgtgag	aacgcctacc	ccggcaacat	650
cacagacacc	atggtgtgtg	ccagcgtgca	ggaagggggc	aaggactcct	700
gccaggggta	ctccgggggc	cctctggtct	gtaaccagtc	tcttcaaggc	750
attatctcct	ggggccagga	tccgtgtgcg	atcacccgaa	agcctggtgt	800
ctacacgaaa	gtctgcaa	atgtggactg	gatccaggag	acgatgaaga	850
acaattagac	tggacccacc	caccacagcc	catcacctc	catttccact	900
tggtgtttgg	ttcctgttca	ctctgtta	aagaaaccct	aagccaagac	950
cctctacgaa	cattctttgg	gcctcctgga	ctacaggaga	tgctgtcact	1000
taataatcaa	cctgggggttc	gaaatcagtg	agacctggat	tcaaattctg	1050
ccttgaaata	ttgtgactct	gggaatgaca	acacctgggt	tgttctctgt	1100
tgtaacccca	gccccaaaga	cagctcctgg	ccatatatca	aggtttcaat	1150
aaatatttgc	taaatgaaaa	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	1200
aaaa	1204				

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<210> 170
<211> 250
<212> PRT
<213> Homo sapiens
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<400> 170
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
  1             5             10             15
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Val	Gly	Gly	Glu	Thr 20	Arg	Ile	Ile	Lys	Gly 25	Phe	Glu	Cys	Lys	Pro 30
His	Ser	Gln	Pro	Trp 35	Gln	Ala	Ala	Leu	Phe 40	Glu	Lys	Thr	Arg	Leu 45
Leu	Cys	Gly	Ala	Thr 50	Leu	Ile	Ala	Pro	Arg 55	Trp	Leu	Leu	Thr	Ala 60
Ala	His	Cys	Leu	Lys 65	Pro	Arg	Tyr	Ile	Val 70	His	Leu	Gly	Gln	His 75
Asn	Leu	Gln	Lys	Glu 80	Glu	Gly	Cys	Glu	Gln 85	Thr	Arg	Thr	Ala	Thr 90
Glu	Ser	Phe	Pro	His 95	Pro	Gly	Phe	Asn	Asn 100	Ser	Leu	Pro	Asn	Lys 105
Asp	His	Arg	Asn	Asp 110	Ile	Met	Leu	Val	Lys 115	Met	Ala	Ser	Pro	Val 120
Ser	Ile	Thr	Trp	Ala 125	Val	Arg	Pro	Leu	Thr 130	Leu	Ser	Ser	Arg	Cys 135
Val	Thr	Ala	Gly	Thr 140	Ser	Cys	Leu	Ile	Ser 145	Gly	Trp	Gly	Ser	Thr 150
Ser	Ser	Pro	Gln	Leu 155	Arg	Leu	Pro	His	Thr 160	Leu	Arg	Cys	Ala	Asn 165
Ile	Thr	Ile	Ile	Glu 170	His	Gln	Lys	Cys	Glu 175	Asn	Ala	Tyr	Pro	Gly 180
Asn	Ile	Thr	Asp	Thr 185	Met	Val	Cys	Ala	Ser 190	Val	Gln	Glu	Gly	Gly 195
Lys	Asp	Ser	Cys	Gln 200	Gly	Asp	Ser	Gly	Gly 205	Pro	Leu	Val	Cys	Asn 210
Gln	Ser	Leu	Gln	Gly 215	Ile	Ile	Ser	Trp	Gly 220	Gln	Asp	Pro	Cys	Ala 225
Ile	Thr	Arg	Lys	Pro 230	Gly	Val	Tyr	Thr	Lys 235	Val	Cys	Lys	Tyr	Val 240
Asp	Trp	Ile	Gln	Glu 245	Thr	Met	Lys	Asn	Asn 250					

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 171
ggctgcgga ctggaagtca tcggg 25

<210> 172
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 172
ctccaggcca tgaggattct gcag 24

<210> 173
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 174
tctgtgatgt tgccggggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 175
cgtgtagaca ccaggctttc gggtg 25

<210> 176
<211> 18
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctggtc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca etc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaaa atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaagg agacctacta aatgccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttgtt cttggtgttg ggcaagtcatt 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt ttgagattg aactttatgc 450
 tgtgacaaaa ggaccacgga gcattgagac atttaaaca atagacatgg 500
 acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550
 gaatttgaaa aagatgagaa gccacgtgac aagtcataatc aggatgcagt 600
 tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650
 ctccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700
 atttctactt ttttttttta gctatttact gtactttatg tataaaacaa 750
 agtcactttt ctccaagttg tatttgctat ttttcccta tgagaagata 800
 ttttgatctc cccaatacat tgattttggt ataataaatg tgaggctggt 850
 ttgcaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
 aaaaaaa 907

<210> 180
 <211> 222
 <212> PRT
 <213> Homo sapiens

<400> 180
 Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe
 1 5 10 15
 Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu
 20 25 30
 Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn
 35 40 45
 Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr
 50 55 60
 Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg
 65 70 75
 Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly
 80 85 90
 Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro
 95 100 105
 Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly
 110 115 120
 Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu
 125 130 135
 Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser
 140 145 150

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 184
 gatgtctgcc accccaag 18

<210> 185
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

<400> 185
 gcatcctgat atgacttgtc acgtggc 27

<210> 186
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 186
 tacaagaggg aagaggagtt gcac 24

<210> 187
 <211> 52
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-52
 <223> Synthetic construct.

<400> 187
 gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50

cc 52

<210> 188
 <211> 573
 <212> DNA
 <213> Homo sapiens

<400> 188
 cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50
 ctctttggag ctgtgactca gaaaaccaa acttctgtg ctaagtgcc 100

cccaaatgct tcctgtgtca ataacactca ctgcacctgc aaccatggat 150
 atactttctgg atctgggcag aaactattca cattcccctt ggagacatgt 200
 aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250
 aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300
 atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350
 ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500
 ttcttgtttc atttcgcgac tgccctctca gtgtttcctg ggatcccctc 550
 ccaaataaag tacttatatt ctc 573

<210> 189
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 189
 Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser
 1 5 10 15
 Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
 20 25 30
 Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
 35 40 45
 Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
 50 55 60
 Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
 65 70

<210> 190
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 190
 agggaccatt gcttcttcca ggcc 24

<210> 191
 <211> 24
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 192
cctgtgctaa gtgccccca aatgcttct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
caagcaggtc atcccccttgg tgaccttcaa agagaagcag agagggcaga 50
ggtagggggg acagggaaag ggtgacctct gagattcccc ttttccccca 100
gactttggaa gtgaccacc atggggctca gcatcttttt gctcctgtgt 150
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
gctcactgca gcggcagcag gtactgggtg cgcctggggg aacacagcct 350
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450
ctgtctgggc tgcgcctgcc cgtccgcgtc accagcagcg ttcaaccct 500
gcccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550
gctggggcat caccaaccac ccacggaacc cattcccga tctgtctcag 600
tgctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
cgggagaatc acgagcaaca tgggtgtgtc aggcggcgtc ccggggcagg 700
atgcctgcca gggtgattct gggggcccc tgggtgtgtg gggagtcctt 750
caaggctctg tgctctgggg gtctgtgggg cctgtggac aagatggcat 800

ccctggagtc tacacctata tttgcaagta tgtggactgg atccggatga 850
tcatgaggaa caactgacct gtttctctca cctccacccc cacccttaa 900
cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950
ccctagctcc actcttggtg gcctgggaac ttcttggaac tttaactcct 1000
gccagccctt ctaagacca cgagcggggt gagagaagtg tgcaatagtc 1050
tggaataaat ataaatgaag gaggggcaaa aaaaaaaaaa a 1091

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<210> 194
<211> 248
<212> PRT
<213> Homo sapiens
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<400> 194														
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Gln	Ala	Ala	Thr	Pro 20	Lys	Ile	Phe	Asn	Gly 25	Thr	Glu	Cys	Gly	Arg 30
Asn	Ser	Gln	Pro	Trp 35	Gln	Val	Gly	Leu	Phe 40	Glu	Gly	Thr	Ser	Leu 45
Arg	Cys	Gly	Gly	Val 50	Leu	Ile	Asp	His	Arg 55	Trp	Val	Leu	Thr	Ala 60
Ala	His	Cys	Ser	Gly 65	Ser	Arg	Tyr	Trp	Val 70	Arg	Leu	Gly	Glu	His 75
Ser	Leu	Ser	Gln	Leu 80	Asp	Trp	Thr	Glu	Gln 85	Ile	Arg	His	Ser	Gly 90
Phe	Ser	Val	Thr	His 95	Pro	Gly	Tyr	Leu	Gly 100	Ala	Ser	Thr	Ser	His 105
Glu	His	Asp	Leu	Arg 110	Leu	Leu	Arg	Leu	Arg 115	Leu	Pro	Val	Arg	Val 120
Thr	Ser	Ser	Val	Gln 125	Pro	Leu	Pro	Leu	Pro 130	Asn	Asp	Cys	Ala	Thr 135
Ala	Gly	Thr	Glu	Cys 140	His	Val	Ser	Gly	Trp 145	Gly	Ile	Thr	Asn	His 150
Pro	Arg	Asn	Pro	Phe 155	Pro	Asp	Leu	Leu	Gln 160	Cys	Leu	Asn	Leu	Ser 165
Ile	Val	Ser	His	Ala 170	Thr	Cys	His	Gly	Val 175	Tyr	Pro	Gly	Arg	Ile 180
Thr	Ser	Asn	Met	Val 185	Cys	Ala	Gly	Gly	Val 190	Pro	Gly	Gln	Asp	Ala 195
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu

200	205	210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp		
215	220	225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp		
230	235	240
Ile Arg Met Ile Met Arg Asn Asn		
245		

<210> 195
 <211> 1485
 <212> DNA
 <213> Homo sapiens

<400> 195
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 ctcgctccctc gccgcgtccg cgaagcctgg agccggcggg agccccgcgc 100
 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcggtc 150
 ggcttgctca aagccccgga ggagaggagg ctggccgaga tcaaccggga 200
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
 caagaccacac ctggagatga agaagatgat ctgagagggtg acaggagggg 400
 tcagtgcacac tatatcttac cgagactttg tgaacatgat gctggggaaa 450
 cggtcggctg tctcaagtt agtcatgatg tttgaaggaa aagccaacga 500
 gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550
 tgccctgagg accccgcctg gactccccag ccttcccacc ccatacctcc 600
 ctcccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650
 tttgtttggt cattgagggg ttgtttgtgt tttcatcaat gtctttgtaa 700
 agcacaaatt atctgcctta aaggggctct gggtcgggga atcctgagcc 750
 ttgggtcccc tccctctctt cttccctcct tccccgctcc ctgtgcagaa 800
 gggctgatat caaaccaaaa actagagggg gcagggccag ggcagggagg 850
 cttccagcct gtgttccccct cacttgaggg aaccagcact ctccatcctt 900
 tcagaaagtc tccaagccaa gttcaggctc actgacctgg ctctgacgag 950
 gacccagggc cactctgaga agaccttggg gtagggacaa ggctgcaggg 1000
 cctctttcgg gtttccttgg acagtgccat ggttccagtg ctctggtgtc 1050

accaggaca cagccactcg gggccccgct gccccagctg atccccactc 1100
 attccacacc tcttctcatc ctcaagtgatg tgaaggtggg aaggaaagga 1150
 gcttggcatt gggagccctt caagaaggta ccagaaggaa ccctccagtc 1200
 ctgctctctg gccacacctg tgcaggcagc tgagaggcag cgtgcagccc 1250
 tactgtccct tactggggca gcagagggct tcggaggcag aagtgaggcc 1300
 tggggtttgg ggggaaaggt cagctcagtg ctgttccacc ttttagggag 1350
 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400
 aagtcagcag cactggtaag ccaagactga gaaatacaag gttgcttgtc 1450
 tgacccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 196
 Met Ser Gly Glu Leu Ser Asn Arg Phe Gln Gly Gly Lys Ala Phe
 1 5 10 15
 Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn
 20 25 30
 Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu
 35 40 45
 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp
 50 55 60
 Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met
 65 70 75
 Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys
 80 85 90
 Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr
 95 100 105
 Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu
 110 115 120
 Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro
 125 130 135
 Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro
 140 145 150

<210> 197
 <211> 4842
 <212> DNA
 <213> Homo sapiens

<400> 197
 cgcgctcccc gcgcgcctcc tcgggctcca cgcgctcttg cccgcagagg 50
 cagcctcctc caggagcggg gccctgcaca ccatggcccc cgggtgggca 100
 ggggtcggcg ccgccgtgcg cgcgcgcctg gcgctggcct tggcgtggc 150
 gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200
 gctccgctgc cagcgtggac tgccacgggc tgggcctccg cgcggttcct 250
 cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataatat 300
 caccaggatc accaagatgg acttcgctgg gctcaagaac ctccgagtct 350
 tgcatctgga agacaaccag gtcagcgtca tcgagagagg cgccttcag 400
 gacctgaagc agctagagcg actgcgcctg aacaagaata agctgcaagt 450
 ccttcagaa ttgcttttcc agagcacgcc gaagctcacc agactagatt 500
 tgagtgaaaa ccagatccag gggatcccga ggaaggcgtt ccgcggcatc 550
 accgatgtga agaacctgca actggacaac aaccacatca gctgcattga 600
 agatggagcc ttccgagcgc tcgcgcgattt ggagatcctt accctcaaca 650
 acaacaacat cagtcgcac ctcgtcacca gcttcaacca catgccgaag 700
 atccgaactc tcgcctcca ctccaaccac ctctactgcg actgccacct 750
 ggcttggtc tcggattggc tcgcacagcg acggacagtt ggccagttca 800
 cactctgcat ggctcctgtg catttgaggg gcttcaacgt ggcggatgtg 850
 cagaagaagg agtacgtgtg ccagccccc cactcggagc cccatcctg 900
 caatgccaac tccatctcct gcccttcgcc ctgcacgtgc agcaataaca 950
 tcgtggactg tcgaggaaag ggcttgatgg agattcctgc caacttgccg 1000
 gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 1050
 tgcaggagcc ttcacccagt acaagaaact gaagcgaata gacatcagca 1100
 agaatcagat atcggatatt gctccagatg ccttcaggg cctgaaatca 1150
 ctcacatcgc tggctcctgta tgggaacaag atcaccgaga ttgccaaggg 1200
 actgtttgat gggctggtgt ccctacagct gctcctcctc aatgccaaca 1250
 agatcaactg cctgcgggtg aacacgtttc aggacctgca gaacctcaac 1300
 ttgctctccc tgtatgacaa caagctgcag accatcagca aggggctctt 1350
 cgcccctctg cagtccatcc agacactcca cttagcccaa aaccatttg 1400
 tgtgcgactg ccacttgaag tggctggccg actacctcca ggacaacccc 1450

atcgagacaa gcggggcccg ctgcagcagc ccgcgccgac tcgccaacaa 1500
 gcgcatcagc cagatcaaga gcaagaagtt ccgctgctca ggctccgagg 1550
 attaccgcag caggttcagc agcgagtgtc tcatggacct cgtgtgcccc 1600
 gagaagtgtc gctgtgaggg cacgattgtg gactgctcca accagaagct 1650
 ggtccgcac ccaagccacc tcctgaata tgtcaccgac ctgcgactga 1700
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 ggaaccagct ggagaccgtg cacgggcgcg tgttccgtgg cctcagtggc 1900
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 cacctttgcc ggctgagtt cggtgagact gctgtccctc tatgacaatc 2000
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 accataaacc tctgttccaa ccccttcaac tgcaactgcc acctggcctg 2100
 gctcggcaag tggttgagga agaggcggat cgtcagtggg aaccctaggt 2150
 gccagaagcc atttttcctc aaggagattc ccatccagga tgtggccatc 2200
 caggacttca cctgtgatgg caacgaggag agtagctgcc agctgagccc 2250
 gcgctgcccc gagcagtga cctgtatgga gacagtgggt cgatgcagca 2300
 acaaggggct ccgcgcctc cccagaggca tgccaagga tgtgaccgag 2350
 ctgtacctgg aaggaaacca cctaacagcc gtgcccagag agctgtccgc 2400
 cctccgacac ctgacgctta ttgacctgag caacaacagc atcagcatgc 2450
 tgaccaatta caccttcagt aacatgtctc acctctccac tctgatcctg 2500
 agctacaacc ggctgaggtg catccccgtc cacgccttca acgggctgcg 2550
 gtccctgcga gtgctaacc tccatggcaa tgacatttcc agcgttcctg 2600
 aaggctcctt caacgacctc acatctcttt cccatctggc gctgggaacc 2650
 aaccactcc actgtgactg cagtcttcgg tggctgtcgg agtgggtgaa 2700
 ggcggggtac aaggagcctg gcacgcctc ctgcagtagc cctgagccca 2750
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 gggccagtgg acatcaacat tgtggccaaa tgcaatgcct gcctctccag 2850
 cccgtgcaag aataacggga catgcacca ggaccctgtg gagctgtacc 2900

gctgtgcctg cccctacagc tacaagggca aggactgcac tgtgcccac 2950
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 tgacagccac aaggatgggt tcagctgctc ctgccctctg ggctttgagg 3050
 ggcagcgggtg tgagatcaac ccagatgact gtgaggacaa cgactgcgaa 3100
 aacaatgccca cctgcgtgga cgggatcaac aactacgtgt gtatctgtcc 3150
 gcctaactac acaggtgagc tatgcgacga ggtgattgac cactgtgtgc 3200
 ctgagctgaa cctctgtcag catgaggcca agtgcacccc cctggacaaa 3250
 ggattcagct gcgagtgtgt ccctggctac agcgggaagc tctgtgagac 3300
 agacaatgat gactgtgtgg ccacaagtg ccgccacggg gccagtgcg 3350
 tggacacaat caatggctac acatgcacct gccccaggg cttcagtgga 3400
 cccttctgtg aacaccccc acccatggtc ctactgcaga ccagcccatg 3450
 cgaccagtac gagtgcaga acggggccca gtgcatcgtg gtgcagcagg 3500
 agcccacctg ccgctgccca ccaggcttcg ccggccccag atgcgagaag 3550
 ctcatcactg tcaacttctg gggcaaagac tcctacgtgg aactggcctc 3600
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 gtgtggagct ggtgacgcta aaccagaccc tgaacctagt agtggacaaa 3850
 ggaactcaa agagcctggg gaagctccag aagcagccag cagtgggcat 3900
 caacagcccc ctctaccttg gaggcacccc cacctccacc ggctctccg 3950
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 catgaggtgc gcatcaacaa cgagctgcag gacttcaagg ccctcccacc 4050
 acagtccttg ggggtgtcac caggctgcaa gtccctgcacc gtgtgcaagc 4100
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 ccaggctgga ccggccact ctgcgaccag gaggcccggtg acccctgcct 4200
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 tgtgcaagtg tgccgagggc tatggagggg acttgtgtga caacaagaat 4300
 gactctgcca atgcctgctc agccttcaag tgtcaccatg ggcagtgcc 4350

catctcagac caaggggagc cctactgcct gtgccagccc ggcttttagcg 4400
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 gtgatccgcc gccagaaagg ttatgcatca tgtgccacag cctccaaggt 4500
 gcccacatg gaatgtcgtg ggggctgtgg gcccagtgcc tgccagccca 4550
 cccgcagcaa gcggcgga aa tacgtcttcc agtgcacgga cggctcctcg 4600
 tttgtagaag aggtggagag acacttagag tgcggctgcc tcgctgttc 4650
 ctaagcccct gccgcctgc ctgccacctc tcggactcca gcttgatgga 4700
 gttgggacag ccatgtggga cccctggtg attcagcatg aaggaaatga 4750
 agctggagag gaaggtaaag aagaagagaa tattaagtat attgtaaaat 4800
 aaacaaaaaa tagaacttaa aaaaaaaaaa aaaaaaaaaa aa 4842

<210> 198
 <211> 1523
 <212> PRT
 <213> Homo sapiens

<400> 198
 Met Ala Pro Gly Trp Ala Gly Val Gly Ala Ala Val Arg Ala Arg
 1 5 10 15
 Leu Ala Leu Ala Leu Ala Leu Ala Ser Val Leu Ser Gly Pro Pro
 20 25 30
 Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val
 35 40 45
 Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro
 50 55 60
 Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg
 65 70 75
 Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu
 80 85 90
 His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe
 95 100 105
 Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys
 110 115 120
 Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu
 125 130 135
 Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg
 140 145 150
 Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp
 155 160 165

Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu	170	175	180
Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Ile Ser Arg	185	190	195
Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu	200	205	210
Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp	215	220	225
Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr	230	235	240
Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp	245	250	255
Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro	260	265	270
Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr	275	280	285
Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu	290	295	300
Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu	305	310	315
Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr	320	325	330
Lys Lys Leu Lys Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp	335	340	345
Ile Ala Pro Asp Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu	350	355	360
Val Leu Tyr Gly Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe	365	370	375
Asp Gly Leu Val Ser Leu Gln Leu Leu Leu Leu Asn Ala Asn Lys	380	385	390
Ile Asn Cys Leu Arg Val Asn Thr Phe Gln Asp Leu Gln Asn Leu	395	400	405
Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ser Lys	410	415	420
Gly Leu Phe Ala Pro Leu Gln Ser Ile Gln Thr Leu His Leu Ala	425	430	435
Gln Asn Pro Phe Val Cys Asp Cys His Leu Lys Trp Leu Ala Asp	440	445	450
Tyr Leu Gln Asp Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Ser			

455										460					465				
Ser	Pro	Arg	Arg	Leu	Ala	Asn	Lys	Arg	Ile	Ser	Gln	Ile	Lys	Ser					
				470					475					480					
Lys	Lys	Phe	Arg	Cys	Ser	Gly	Ser	Glu	Asp	Tyr	Arg	Ser	Arg	Phe					
				485					490					495					
Ser	Ser	Glu	Cys	Phe	Met	Asp	Leu	Val	Cys	Pro	Glu	Lys	Cys	Arg					
				500					505					510					
Cys	Glu	Gly	Thr	Ile	Val	Asp	Cys	Ser	Asn	Gln	Lys	Leu	Val	Arg					
				515					520					525					
Ile	Pro	Ser	His	Leu	Pro	Glu	Tyr	Val	Thr	Asp	Leu	Arg	Leu	Asn					
				530					535					540					
Asp	Asn	Glu	Val	Ser	Val	Leu	Glu	Ala	Thr	Gly	Ile	Phe	Lys	Lys					
				545					550					555					
Leu	Pro	Asn	Leu	Arg	Lys	Ile	Asn	Leu	Ser	Asn	Asn	Lys	Ile	Lys					
				560					565					570					
Glu	Val	Arg	Glu	Gly	Ala	Phe	Asp	Gly	Ala	Ala	Ser	Val	Gln	Glu					
				575					580					585					
Leu	Met	Leu	Thr	Gly	Asn	Gln	Leu	Glu	Thr	Val	His	Gly	Arg	Val					
				590					595					600					
Phe	Arg	Gly	Leu	Ser	Gly	Leu	Lys	Thr	Leu	Met	Leu	Arg	Ser	Asn					
				605					610					615					
Leu	Ile	Ser	Cys	Val	Ser	Asn	Asp	Thr	Phe	Ala	Gly	Leu	Ser	Ser					
				620					625					630					
Val	Arg	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Arg	Ile	Thr	Thr	Ile	Thr					
				635					640					645					
Pro	Gly	Ala	Phe	Thr	Thr	Leu	Val	Ser	Leu	Ser	Thr	Ile	Asn	Leu					
				650					655					660					
Leu	Ser	Asn	Pro	Phe	Asn	Cys	Asn	Cys	His	Leu	Ala	Trp	Leu	Gly					
				665					670					675					
Lys	Trp	Leu	Arg	Lys	Arg	Arg	Ile	Val	Ser	Gly	Asn	Pro	Arg	Cys					
				680					685					690					
Gln	Lys	Pro	Phe	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp	Val	Ala					
				695					700					705					
Ile	Gln	Asp	Phe	Thr	Cys	Asp	Gly	Asn	Glu	Glu	Ser	Ser	Cys	Gln					
				710					715					720					
Leu	Ser	Pro	Arg	Cys	Pro	Glu	Gln	Cys	Thr	Cys	Met	Glu	Thr	Val					
				725					730					735					
Val	Arg	Cys	Ser	Asn	Lys	Gly	Leu	Arg	Ala	Leu	Pro	Arg	Gly	Met					
				740					745					750					

Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr	755	760	765
Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile	770	775	780
Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe	785	790	795
Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg	800	805	810
Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu	815	820	825
Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu	830	835	840
Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly	845	850	855
Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu	860	865	870
Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser	875	880	885
Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu Thr Thr Pro Thr	890	895	900
His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala	905	910	915
Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr	920	925	930
Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr	935	940	945
Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile	950	955	960
Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser	965	970	975
His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly	980	985	990
Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys	995	1000	1005
Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys	1010	1015	1020
Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile	1025	1030	1035
Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys			

1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly		
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala		
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly		
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu		
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln		
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu		
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu		
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu		
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln		
1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser
 1340 1345 1350
 Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
 1355 1360 1365
 Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
 1370 1375 1380
 Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
 1385 1390 1395
 Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
 1400 1405 1410
 Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
 1415 1420 1425
 Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
 1430 1435 1440
 Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
 1445 1450 1455
 Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala
 1460 1465 1470
 Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
 1475 1480 1485
 Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
 1490 1495 1500
 Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu
 1505 1510 1515
 Glu Cys Gly Cys Leu Ala Cys Ser
 1520

<210> 199
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 199
 atggagattc ctgccaaactt gccg 24

<210> 200
 <211> 24
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 200
 ttgttgcat tgaggaggag cagc 24

<210> 201
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 201
 gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202
 <211> 753
 <212> DNA
 <213> Homo sapiens

<400> 202
 ggatgcagga cgctcccctg agctgcctgt caccgactag gtggagcagt 50
 gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100
 gaatctgcct ttccagttct gtctccggca ggctttgagg atgaaggctg 150
 cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200
 atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250
 caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300
 agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350
 gactatggca tcttcagat caacagcttc gcgtggtgca gacgcggaaa 400
 gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450
 atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500
 caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550
 cctgtccgag tggaaaaaag gctgtgaggt ttcttaaact ggaactggac 600
 ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650
 cctgtgtcat cttgtcccgt ttctcccaa tttccttctt caaacttgga 700
 gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaaatt 750
 gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 203
 Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr
 1 5 10 15
 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
 20 25 30
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
 125 130 135
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
 140 145

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 204
 gcaggctttg aggatgaagg ctgc 24

<210> 205
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 205
ctcattggct gcctgggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgacca aggctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 208
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<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
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tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaagaag atcctatattt actgtcactt ccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300
 gaggaatata ccacagggcat ggcagactgc atcttagtca acagccagtt 350
 cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400
 ctgatgtcct ctatccatct ctaaattgtca ccagctttga ctgagttgtt 450
 cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500
 ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcactggaag 550
 ccctagtaca gctgcgtgga agattgacat cccaagattg ggagaggggtt 600
 catctgatcg tggcaggtgg ttatgacgag agagtcctgg agaattgtga 650
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 atgtgacctt cttgaggtct ttctcagaca aacagaaaat ctccctcctc 750
 cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800
 tgtccctctg gaagccatgt acatgcagtg ccagtcatt gctgttaatt 850
 cgggtggacc cttggagtc attgaccaca gtgtcacagg gtttctgtgt 900
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 tcaactgcat ctgttaggga atttttgttt gtccctgtctt tgcctggatc 1550
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 actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaaaa 1648

<210> 210

<211> 323

<212> PRT
<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	1	5	10	15
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	20	25	30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	35	40	45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	50	55	60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	65	70	75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	80	85	90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	95	100	105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	110	115	120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	125	130	135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	140	145	150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	155	160	165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	170	175	180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	185	190	195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	200	205	210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	215	220	225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	230	235	240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	245	250	255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	260	265	270	

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg
275 280 285

Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg
290 295 300

Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr
305 310 315

Arg Tyr Val Thr Lys Leu Leu Val
320

<210> 211
<211> 1554
<212> DNA
<213> Homo sapiens

<400> 211
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tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag 200
tttgcatagag ttctctggtta atttgcatag gagatatggg cctgtggtct 250
ccttctggtt tggcaggcgc ctcgtggtta gtttgggcac tgttgatgta 300
ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350
gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaaa 400
accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500
gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
gttttgctat gaagtctggt acacagatgg taatgggtag tacatttgaa 600
gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650
tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700
ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
aacatcataa aagaacgaaa aggaaggaaac ttcagtcaac atattttcat 800
tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850
gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950
tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tggtcgaact 1050
 gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100
 tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150
 tgggtacttca ggatcctaact acttggccat ctccacacaa gtttgatcca 1200
 gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggatt 1250
 ctcaggcaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300
 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350
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 agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450
 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550
 ttaa 1554

<210> 212
 <211> 462
 <212> PRT
 <213> Homo sapiens

<400> 212
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 Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala
 20 25 30
 Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu
 35 40 45
 Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn
 50 55 60
 Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg
 65 70 75
 Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His
 80 85 90
 Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys
 95 100 105
 Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn
 110 115 120
 His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu
 125 130 135
 Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu

140										145					150				
Asp	Lys	Trp	Leu	Ser	Tyr	Pro	Glu	Thr	Gln	His	Val	Pro	Leu	Ser					
				155					160					165					
Gln	His	Met	Leu	Gly	Phe	Ala	Met	Lys	Ser	Val	Thr	Gln	Met	Val					
				170					175					180					
Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln	Glu	Val	Ile	Arg	Phe	Gln					
				185					190					195					
Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile	Gly	Lys	Gly	Phe	Leu					
				200					205					210					
Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys	Lys	Gln	Tyr	Glu					
				215					220					225					
Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn	Ile	Ile	Lys					
				230					235					240					
Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	Asp	Ser					
				245					250					255					
Leu	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	Ser					
				260					265					270					
Met	Ile	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys					
				275					280					285					
Thr	Trp	Ala	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys					
				290					295					300					
Lys	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val					
				305					310					315					
Thr	Pro	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu					
				320					325					330					
Cys	Glu	Thr	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln					
				335					340					345					
Leu	Gln	Asp	Ile	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg					
				350					355					360					
Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro					
				365					370					375					
Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp					
				380					385					390					
Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly					
				395					400					405					
Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr	Met	Val	Thr	Thr					
				410					415					420					
Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu	Leu	Ser	Val					
				425					430					435					

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
455 460

<210> 213
<211> 759
<212> DNA
<213> Homo sapiens

<400> 213
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tcagggcttg tgccctctcg cttcctgacg ctcttgccgc atctggtggt 150
cgatcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200
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gggctcactg tagtgcaccc gtggccctgt ccttcttcat attcgagcgt 400
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ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcgggt 600
ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650
tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700
tgttttgtag taacattaag acttatatac agtttttaggg gacaattaa 750
aaaaaaaa 759

<210> 214
<211> 140
<212> PRT
<213> Homo sapiens

<400> 214
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Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
20 25 30
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
35 40 45

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
 50 55 60
 Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
 65 70 75
 Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
 80 85 90
 Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
 95 100 105
 Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
 110 115 120
 Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
 125 130 135
 Lys Lys Lys Pro Phe
 140

<210> 215
 <211> 697
 <212> DNA
 <213> Homo sapiens

<400> 215
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 gacccggcct gctgcagccc catagtcccc cggaacgagt ggaaggccct 150
 ggcacagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200
 tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
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 catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216
 <211> 196
 <212> PRT

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ctttggtggt ggggacttct actccaacat caagacgggtg gccctgaacc 400
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gaacgggggc gccggacctc gctttgcacc cagcaccag ccaagatctg 650
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ctcctctggg agcatccatg tcccgagag ggtccctca acagtacgcc 1650

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200
gcgccgccgc cgccgtcgct cctgcagcgc tgtcgaccta gccgctagca 250
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agcgccagcc ggctgcggct gccacacagg ctcaccatgg gctccgggcg 350
ccgggcgctg tccgcggtgc cggccgtgct gctggtcctc acgctgccgg 400
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aagacgcgca tcatttactt cgatcagatc ctggtgaatg tgggtaattt 650
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tcagttttca cgtgattaaa gtctaccaga gccaaactat ccaggttaac 750
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ttctccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000
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ggtggaatg gattctaagg attctagcct gtctgaacca atacaaaatt 1100

tcacagatta	tttgtgtgtg	tctgtttcag	tatatattgga	ttggggactct	1150
aagcagataa	tacctatgct	taaatgtaac	agtcaaaagc	tgtctgcaag	1200
acttattctg	aatttcattt	cctggggatta	ctgaattagt	tacagatgtg	1250
gaattttatt	tgtttagttt	taaaagactg	gcaaccaggt	ctaaggatta	1300
gaaaactcta	aagttctgac	ttcaatcaac	ggttagtgtg	atactgccaa	1350
agaactgtat	actgtgttaa	tatattgatt	atatttgttt	ttattccttt	1400
ggaattagtt	tgtttggttc	ttgtaaaaaa	cttggaattt	ttttttcagt	1450
aactgggtatt	atgttttctc	ttaaaataag	gtaatgaatg	gcttgcccac	1500
aaatttacct	tgactacgat	atcatcgaca	tgacttctct	caaaaaaaaa	1550
gaatgcttca	tagttgtatt	ttaattgtat	atgtgaaaga	gtcatatttt	1600
ccaagttata	ttttctaaga	agaagaatag	atcataaatc	tgacaaggaa	1650
aaagttgctt	acccaaaatc	taagtgtctc	atccctgagc	ctcagcaaaa	1700
cagctcccct	ccgagggaaa	tcttatactt	tattgctcaa	ctttaattaa	1750
aatgattgat	aataaccact	ttattaaaaa	cctaaggttt	tttttttttc	1800
cgtagacatg	accactttat	taactgggtg	tgggatgctg	ttgtttctaa	1850
ttatacctat	ttttcaaggc	ttctgttgta	tttgaagtat	catctggttt	1900
tgctttaact	ctttaaattg	tatatattta	tctgttttagc	taatattaaa	1950
ttcaaatatc	ccatatctaa	athtagtgca	atatcttgtc	ttttgtatag	2000
gtcatatgaa	ttcataaaat	tatttatgtc	tgttatagaa	taaagattaa	2050
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<210> 220
<211> 201
<212> PRT
<213> Homo sapiens
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<400> 220
Met Gly Ser Gly Arg Arg Ala Leu Ser Ala Val Pro Ala Val Leu
  1          5          10          15

Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp
          20          25          30

Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp
          35          40          45

Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu
          50          55          60

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Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	
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Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	
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Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	
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Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	
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Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	
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Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	
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Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	
				170					175					180	
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	
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 <212> DNA
 <213> Artificial

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 <223> Synthetic construct.

<400> 221
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<400> 222
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<210> 223
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<212> DNA
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<220>
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<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

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<211> 257
<212> PRT

<211> 3939
 <212> DNA
 <213> Homo sapiens

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<210> 227
<211> 832
<212> PRT
<213> Homo sapiens
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<400> 227

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Val Glu Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gln
20 25 30

Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser
 35 40 45
 Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn
 50 55 60
 Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys Gln
 65 70 75
 Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val
 80 85 90
 Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg
 95 100 105
 Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro
 110 115 120
 Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser
 125 130 135
 Thr Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg
 140 145 150
 Met Asp Asp Phe Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn
 155 160 165
 Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu
 170 175 180
 Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn Lys Ala Phe
 185 190 195
 Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro Val Tyr
 200 205 210
 Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr Met
 215 220 225
 Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
 230 235 240
 Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala
 245 250 255
 Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro
 260 265 270
 Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser
 275 280 285
 Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys
 290 295 300
 Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala
 305 310 315
 Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala

320	325	330
Ile Asp Arg Ala Cys Pro Glu Ser Gly	His Pro Arg Val Leu Ala	
335	340	345
Asp Ser Phe Pro Gly Ser Ser Pro Tyr	Glu Gly Tyr Asn Tyr Gly	
350	355	360
Ser Phe Glu Asn Val Ser Gly Ser Thr	Asp Gly Leu Val Asp Ser	
365	370	375
Ala Gly Thr Gly Asp Leu Ser Tyr Gly	Tyr Gln Gly Arg Ser Phe	
380	385	390
Glu Pro Val Gly Thr Arg Pro Arg Val	Asp Ser Met Ser Ser Val	
395	400	405
Glu Glu Asp Asp Tyr Asp Thr Leu Thr	Asp Ile Asp Ser Asp Lys	
410	415	420
Asn Val Ile Arg Thr Lys Gln Tyr Leu	Tyr Val Ala Asp Leu Ala	
425	430	435
Arg Lys Asp Lys Arg Val Leu Arg Lys	Lys Tyr Gln Ile Tyr Phe	
440	445	450
Trp Asn Ile Ala Thr Ile Ala Val Phe	Tyr Ala Leu Pro Val Val	
455	460	465
Gln Leu Val Ile Thr Tyr Gln Thr Val	Val Asn Val Thr Gly Asn	
470	475	480
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu	Cys Ala His Pro Leu Gly	
485	490	495
Asn Leu Ser Ala Phe Asn Asn Ile Leu	Ser Asn Leu Gly Tyr Ile	
500	505	510
Leu Leu Gly Leu Leu Phe Leu Leu Ile	Ile Leu Gln Arg Glu Ile	
515	520	525
Asn His Asn Arg Ala Leu Leu Arg Asn	Asp Leu Cys Ala Leu Glu	
530	535	540
Cys Gly Ile Pro Lys His Phe Gly Leu	Phe Tyr Ala Met Gly Thr	
545	550	555
Ala Leu Met Met Glu Gly Leu Leu Ser	Ala Cys Tyr His Val Cys	
560	565	570
Pro Asn Tyr Thr Asn Phe Gln Phe Asp	Thr Ser Phe Met Tyr Met	
575	580	585
Ile Ala Gly Leu Cys Met Leu Lys Leu	Tyr Gln Lys Arg His Pro	
590	595	600
Asp Ile Asn Ala Ser Ala Tyr Ser Ala	Tyr Ala Cys Leu Ala Ile	
605	610	615

Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn
 620 625 630
 Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr
 635 640 645
 Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu
 650 655 660
 Asp Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp
 665 670 675
 Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val
 680 685 690
 Leu Leu Val Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr
 695 700 705
 Gly Leu Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala
 710 715 720
 Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile
 725 730 735
 Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu
 740 745 750
 Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu Phe Phe
 755 760 765
 Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu Ser
 770 775 780
 Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
 785 790 795
 His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser
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 815 820 825
 Arg Asp Lys Ile Tyr Val Phe
 830

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 <211> 2848
 <212> DNA
 <213> Homo sapiens

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<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

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Leu Pro Arg Glu Gly Ala Glu Gly Gln Ile Val Leu Ser Gly Asp	50		55		60
Ser Gly Lys Ala Thr Glu Gly Pro Phe Ala Met Asp Pro Asp Ser	65		70		75
Gly Phe Leu Leu Val Thr Arg Ala Leu Asp Arg Glu Glu Gln Ala	80		85		90
Glu Tyr Gln Leu Gln Val Thr Leu Glu Met Gln Asp Gly His Val	95		100		105
Leu Trp Gly Pro Gln Pro Val Leu Val His Val Lys Asp Glu Asn	110		115		120
Asp Gln Val Pro His Phe Ser Gln Ala Ile Tyr Arg Ala Arg Leu	125		130		135
Ser Arg Gly Thr Arg Pro Gly Ile Pro Phe Leu Phe Leu Glu Ala	140		145		150
Ser Asp Arg Asp Glu Pro Gly Thr Ala Asn Ser Asp Leu Arg Phe	155		160		165
His Ile Leu Ser Gln Ala Pro Ala Gln Pro Ser Pro Asp Met Phe	170		175		180
Gln Leu Glu Pro Arg Leu Gly Ala Leu Ala Leu Ser Pro Lys Gly	185		190		195
Ser Thr Ser Leu Asp His Ala Leu Glu Arg Thr Tyr Gln Leu Leu	200		205		210
Val Gln Val Lys Asp Met Gly Asp Gln Ala Ser Gly His Gln Ala	215		220		225
Thr Ala Thr Val Glu Val Ser Ile Ile Glu Ser Thr Trp Val Ser	230		235		240
Leu Glu Pro Ile His Leu Ala Glu Asn Leu Lys Val Leu Tyr Pro	245		250		255
His His Met Ala Gln Val His Trp Ser Gly Gly Asp Val His Tyr	260		265		270
His Leu Glu Ser His Pro Pro Gly Pro Phe Glu Val Asn Ala Glu	275		280		285
Gly Asn Leu Tyr Val Thr Arg Glu Leu Asp Arg Glu Ala Gln Ala	290		295		300
Glu Tyr Leu Leu Gln Val Arg Ala Gln Asn Ser His Gly Glu Asp	305		310		315

Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn
				320					325					330
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile
				335					340					345
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala
				350					355					360
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr
				365					370					375
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala
				380					385					390
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu
				395					400					405
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met
				410					415					420
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val
				425					430					435
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile
				440					445					450
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro
				455					460					465
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu
				470					475					480
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr
				485					490					495
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val
				500					505					510
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser
				515					520					525
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly
				530					535					540
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val
				545					550					555
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu
				560					565					570
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr
				575					580					585
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu
				590					595					600
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly

				605					610					615
Glu	Val	His	Thr	Ala 620	Gln	Ser	Leu	Gln	Gly 625	Ala	Gln	Pro	Gly	Asp 630
Thr	Tyr	Thr	Val	Leu 635	Val	Glu	Ala	Gln	Asp 640	Thr	Ala	Leu	Thr	Leu 645
Ala	Pro	Val	Pro	Ser 650	Gln	Tyr	Leu	Cys	Thr 655	Pro	Arg	Gln	Asp	His 660
Gly	Leu	Ile	Val	Ser 665	Gly	Pro	Ser	Lys	Asp 670	Pro	Asp	Leu	Ala	Ser 675
Gly	His	Gly	Pro	Tyr 680	Ser	Phe	Thr	Leu	Gly 685	Pro	Asn	Pro	Thr	Val 690
Gln	Arg	Asp	Trp	Arg 695	Leu	Gln	Thr	Leu	Asn 700	Gly	Ser	His	Ala	Tyr 705
Leu	Thr	Leu	Ala	Leu 710	His	Trp	Val	Glu	Pro 715	Arg	Glu	His	Ile	Ile 720
Pro	Val	Val	Val	Ser 725	His	Asn	Ala	Gln	Met 730	Trp	Gln	Leu	Leu	Val 735
Arg	Val	Ile	Val	Cys 740	Arg	Cys	Asn	Val	Glu 745	Gly	Gln	Cys	Met	Arg 750
Lys	Val	Gly	Arg	Met 755	Lys	Gly	Met	Pro	Thr 760	Lys	Leu	Ser	Ala	Val 765
Gly	Ile	Leu	Val	Gly 770	Thr	Leu	Val	Ala	Ile 775	Gly	Ile	Phe	Leu	Ile 780
Leu	Ile	Phe	Thr	His 785	Trp	Thr	Met	Ser	Arg 790	Lys	Lys	Asp	Pro	Asp 795
Gln	Pro	Ala	Asp	Ser 800	Val	Pro	Leu	Lys	Ala 805	Thr	Val			

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<210> 230
<211> 50
<212> DNA
<213> Artificial
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<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 230
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<210> 231
<211> 24
<212> DNA
<213> Artificial Sequeunce
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<220>
<221> Artificial Sequence
<222> full
<223> Synthetic oligonucleotide probe

<400> 231
cctgagctgt aacccactc cagg 24

<210> 232
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 232
agagtctgtc ccagctatct tgt 23

<210> 233
<211> 2786
<212> DNA
<213> Homo sapiens

<400> 233
ccggggacat gaggtggata ctgttcattg gggcccttat tgggtccagc 50
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cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150
acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200
gatgtcctgg tcccatctgt cagtctgcag gcattttaat ccttcctgag 250
atcccagggc ttagagtacg cagtgcacat tgaggacctg caggcccttt 300
tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350
agtaataact tcaactacgg ggcttaccat tccctggaag ctattttacca 400
cgagatggac aacattgccg cagactttcc tgacctggcg aggaggggtga 450
agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500
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gctcctgcat tgggtgctgac ccaaatagaa actggaacgc tagttttgca 800
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<210> 234
 <211> 421
 <212> PRT
 <213> Homo sapiens

<400> 234
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 1 5 10 15
 Cys Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Leu Arg Ile Asn
 20 25 30
 Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn
 35 40 45
 Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe
 50 55 60
 Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala
 65 70 75
 Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr
 80 85 90
 Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met
 95 100 105
 Gln His Asn Glu Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr
 110 115 120
 Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn
 125 130 135
 Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly
 140 145 150
 His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr
 155 160 165

Gly Lys Gly Val	Arg Arg Pro Ala Val	Trp Leu Asn Ala Gly Ile
170		175 180
His Ser Arg Glu	Trp Ile Ser Gln Ala	Thr Ala Ile Trp Thr Ala
185		190 195
Arg Lys Ile Val	Ser Asp Tyr Gln Arg	Asp Pro Ala Ile Thr Ser
200		205 210
Ile Leu Glu Lys	Met Asp Ile Phe Leu	Leu Pro Val Ala Asn Pro
215		220 225
Asp Gly Tyr Val	Tyr Thr Gln Thr Gln	Asn Arg Leu Trp Arg Lys
230		235 240
Thr Arg Ser Arg	Asn Pro Gly Ser Ser	Cys Ile Gly Ala Asp Pro
245		250 255
Asn Arg Asn Trp	Asn Ala Ser Phe Ala	Gly Lys Gly Ala Ser Asp
260		265 270
Asn Pro Cys Ser	Glu Val Tyr His Gly	Pro His Ala Asn Ser Glu
275		280 285
Val Glu Val Lys	Ser Val Val Asp Phe	Ile Gln Lys His Gly Asn
290		295 300
Phe Lys Gly Phe	Ile Asp Leu His Ser	Tyr Ser Gln Leu Leu Met
305		310 315
Tyr Pro Tyr Gly	Tyr Ser Val Lys Lys	Ala Pro Asp Ala Glu Glu
320		325 330
Leu Asp Lys Val	Ala Arg Leu Ala Ala	Lys Ala Leu Ala Ser Val
335		340 345
Ser Gly Thr Glu	Tyr Gln Val Gly Pro	Thr Cys Thr Thr Val Tyr
350		355 360
Pro Ala Ser Gly	Ser Ser Ile Asp Trp	Ala Tyr Asp Asn Gly Ile
365		370 375
Lys Phe Ala Phe	Thr Phe Glu Leu Arg	Asp Thr Gly Thr Tyr Gly
380		385 390
Phe Leu Leu Pro	Ala Asn Gln Ile Ile	Pro Thr Ala Glu Glu Thr
395		400 405
Trp Leu Gly Leu	Lys Thr Ile Met Glu	His Val Arg Asp Asn Leu
410		415 420

Tyr

<210> 235
 <211> 1743
 <212> DNA
 <213> Homo sapiens

<400> 235

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 cccgcccttc ctccacaaag agcaccctg cctcacaggt gtattccctc 200
 aacaccgact ttgccttccg cctataccgc aggctggttt tggagacccc 250
 gagtcagaac atcttcttct cccctgtgag tgtctccact tccctggcca 300
 tgctctccct tggggccac tcagtcacca agaccagat tctccagggc 350
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 cactaaatcc taggtgggaa atggcctgtt aactgatggc acattgctaa 1350
 tgcacaagaa ataacaaacc acatccctct ttctgttctg aggggtgcatt 1400
 tgacccagct ggagctggat tcgctggcag ggatgccact tccaaggctc 1450

aatcaccaaa ccatcaacag ggacccagc cacaagccaa cacccattaa 1500
 cccagtcag tgcccttttc cacaaattct cccaggtaac tagcttcag 1550
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 236
 Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu Cys
 1 5 10 15
 Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr
 20 25 30
 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr
 35 40 45
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
 50 55 60
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val
 65 70 75
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr
 80 85 90
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr
 95 100 105
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser
 110 115 120
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala
 125 130 135
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly
 140 145 150
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe
 155 160 165
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys
 170 175 180
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp
 185 190 195
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala

200	205	210
Lys Trp Glu Lys Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn Phe	
215	220	225
Pro Phe Leu Val Gly Glu Gln Val Thr	Val Gln Val Pro Met Met	
230	235	240
His Gln Lys Glu Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu Asn	
245	250	255
Cys Phe Val Leu Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala Phe	
260	265	270
Phe Val Leu Pro Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln Ala	
275	280	285
Leu Ser Ala Arg Thr Leu Ile Lys Trp	Ser His Ser Leu Gln Lys	
290	295	300
Arg Trp Ile Glu Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala Ser	
305	310	315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn Ala	
320	325	330
Phe Asp Lys Asn Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp Ser	
335	340	345
Leu Gln Val Ser Lys Ala Thr His Lys	Ala Val Leu Asp Val Ser	
350	355	360
Glu Glu Gly Thr Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe Ile	
365	370	375
Val Arg Ser Lys Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe Asn	
380	385	390
Arg Thr Phe Leu Met Met Ile Thr Asn	Lys Ala Thr Asp Gly Ile	
395	400	405
Leu Phe Leu Gly Lys Val Glu Asn Pro	Thr Lys Ser	
410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 238
ctttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 239
tgactcgggg tctccaaaac cagc 24

<210> 240
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 240
ggtataggcg gaaggcaaag tcgg 24

<210> 241
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 241
ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 242
ggctgaccgt gctacattgc ctggaggaag cctaaggaac ccaggcatcc 50

agctgccac gcctgagtcc aagattcttc ccaggaacac aaacgtagga 100
gacccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150
ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200
ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250
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aacaattcc aatgagacta gcacctctgc caacctgga tccagtgtga 350
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gcacagccac caactctgag tccagaacga cctccaatgg ggctggcaca 1000
gccaccaact ctgagtccag cacgacctcc agtggggcca gcacagccac 1050
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gcactgccac caactctgag tccagcaca cctccagtgg ggtcagcaca 1450
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cattcatccc aggagacccc tcccagcttt gtttgagatc ctgaaaatct 2150
tgaagaaggt attcctcacc tttcttgctt ttaccagaca ctggaaagag 2200
aatactatat tgctcattta gctaagaaat aaatacatct catctaacac 2250
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gatgaactca gttataggag aaaacctcca tgctggactc catctggcat 2350
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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243
<211> 596
<212> PRT
<213> Homo sapiens

<400> 243
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Leu His Leu Glu Ala Ala Thr Asn Ser Asn Glu Thr Ser Thr Ser
20 25 30
Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala
35 40 45
Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala
50 55 60
Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val
65 70 75

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala
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Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala
				95					100					105
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				110					115					120
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val
				125					130					135
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				140					145					150
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala
				155					160					165
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				170					175					180
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				185					190					195
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				200					205					210
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala
				215					220					225
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				230					235					240
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala
				245					250					255
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				260					265					270
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				275					280					285
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				290					295					300
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				305					310					315
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala
				320					325					330
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val
				335					340					345
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala
				350					355					360
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala

				365					370					375
Thr	Asn	Ser	Glu	Ser 380	Ser	Thr	Val	Ser	Ser 385	Gly	Ala	Ser	Thr	Ala 390
Thr	Asn	Ser	Glu	Ser 395	Ser	Thr	Thr	Ser	Ser 400	Gly	Val	Ser	Thr	Ala 405
Thr	Asn	Ser	Glu	Ser 410	Ser	Thr	Thr	Ser	Ser 415	Gly	Ala	Ser	Thr	Ala 420
Thr	Asn	Ser	Asp	Ser 425	Ser	Thr	Thr	Ser	Ser 430	Glu	Ala	Ser	Thr	Ala 435
Thr	Asn	Ser	Glu	Ser 440	Ser	Thr	Val	Ser	Ser 445	Gly	Ile	Ser	Thr	Val 450
Thr	Asn	Ser	Glu	Ser 455	Ser	Thr	Thr	Ser	Ser 460	Gly	Ala	Asn	Thr	Ala 465
Thr	Asn	Ser	Gly	Ser 470	Ser	Val	Thr	Ser	Ala 475	Gly	Ser	Gly	Thr	Ala 480
Ala	Leu	Thr	Gly	Met 485	His	Thr	Thr	Ser	His 490	Ser	Ala	Ser	Thr	Ala 495
Val	Ser	Glu	Ala	Lys 500	Pro	Gly	Gly	Ser	Leu 505	Val	Pro	Trp	Glu	Ile 510
Phe	Leu	Ile	Thr	Leu 515	Val	Ser	Val	Val	Ala 520	Ala	Val	Gly	Leu	Phe 525
Ala	Gly	Leu	Phe	Phe 530	Cys	Val	Arg	Asn	Ser 535	Leu	Ser	Leu	Arg	Asn 540
Thr	Phe	Asn	Thr	Ala 545	Val	Tyr	His	Pro	His 550	Gly	Leu	Asn	His	Gly 555
Leu	Gly	Pro	Gly	Pro 560	Gly	Gly	Asn	His	Gly 565	Ala	Pro	His	Arg	Pro 570
Arg	Trp	Ser	Pro	Asn 575	Trp	Phe	Trp	Arg	Arg 580	Pro	Val	Ser	Ser	Ile 585
Ala	Met	Glu	Met	Ser 590	Gly	Arg	Asn	Ser	Gly 595	Pro				

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<210> 244
<211> 26
<212> DNA
<213> Artificial
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<220>  
<221> Artificial Sequence  
<222> 1-26  
<223> Synthetic construct.
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<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic sequence.

<400> 245
 gtcagagttg gtggctgtgc tagc 24

<210> 246
 <211> 48
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.

<400> 246
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<210> 247
 <211> 957
 <212> DNA
 <213> Homo sapiens

<400> 247
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 tccctccttc tgctactggg ggccctgtct ggatgggcgg ccagcgatga 150
 ccccatcgag aaggctcattg aagggatcaa ccgagggctg agcaatgcag 200
 agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250
 gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300
 ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350
 tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaag 400
 gaagcagaga agcttgGCCa tggggTcaac aacgctgctg gacaggccgg 450
 gaaggaagca gacaaagcgg tocaaggggt ccacactggg gtccaccagg 500
 ctgggaagga agcagagaaa cttggccaag ggtcaacca tgctgctgac 550
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tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650
ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700
tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750
agtcaacacg cctttcatca accttcccgc cctgtggagg agcgtcgcca 800
acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850
gttgtcacat cagctgacat gacctggagg gggtgggggt gggggacagg 900
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tacacca 957

<210> 248
<211> 247
<212> PRT
<213> Homo sapiens

<400> 248
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Leu Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu
20 25 30
Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg
35 40 45
Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His
50 55 60
Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met
65 70 75
Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu
80 85 90
Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile
95 100 105
Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn
110 115 120
Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln
125 130 135
Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys
140 145 150
Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu
155 160 165
Val Glu Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala
170 175 180

Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
185 190 195

Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
200 205 210

Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly
215 220 225

Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
230 235 240

Ser Val Ala Asn Ile Met Pro
245

<210> 249

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 249

caatatgcat cttgcacgtc tgg 23

<210> 250

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 250

aagcttctct gcttcctttc ctgc 24

<210> 251

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 251

tgacccatt gagaagggtca ttgaagggat caaccgaggg ctg 43

<210> 252

<211> 3781

<212> DNA

<213> Homo sapiens

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cagtggacac	tccaggaaga	gcggccccgc	ggggggcgat	gaccgtgcgc	100
tgaccctgac	tactccagg	tccggaggcg	ggggcccccg	gggcgactcg	150
ggggcggacc	gcggggcgga	gctgccgccc	gtgagtccgg	ccgagccacc	200
tgagcccag	ccgcgggaca	ccgtcgctcc	tgctctccga	atgctgcgca	250
ccgcgatggg	cctgaggagc	tggctcgccc	ccccatgggg	cgcgctgccg	300
cctcgccac	cgctgctgct	gctcctgctg	ctgctgctcc	tgctgcagcc	350
gccgcctccg	acctgggccc	tcagcccccg	gatcagcctg	cctctgggct	400
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cccgggaaag gaagatcaac tcatccctgc agctcccaga ccgcgtgctg 1500
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<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro
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Trp Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu Leu
20 25 30

Leu Leu Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser
35 40 45

Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu
50 55 60

Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu
65 70 75

Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

80										85					90				
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr					
				95					100					105					
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys					
				110					115					120					
Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile					
				125					130					135					
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly					
				140					145					150					
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn					
				155					160					165					
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp					
				170					175					180					
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala					
				185					190					195					
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe					
				200					205					210					
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro					
				215					220					225					
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe					
				230					235					240					
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly					
				245					250					255					
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu					
				260					265					270					
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile					
				275					280					285					
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp					
				290					295					300					
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp					
				305					310					315					
Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro					
				320					325					330					
Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr					
				335					340					345					
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val					
				350					355					360					
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys					
				365					370					375					

Glu	Val	Asn	Arg	Glu 380	Thr	Gln	Gln	Trp	Tyr 385	Thr	Val	Thr	His	Pro 390
Val	Pro	Thr	Pro	Arg 395	Pro	Gly	Ala	Cys	Ile 400	Thr	Asn	Ser	Ala	Arg 405
Glu	Arg	Lys	Ile	Asn 410	Ser	Ser	Leu	Gln	Leu 415	Pro	Asp	Arg	Val	Leu 420
Asn	Phe	Leu	Lys	Asp 425	His	Phe	Leu	Met	Asp 430	Gly	Gln	Val	Arg	Ser 435
Arg	Met	Leu	Leu	Leu 440	Gln	Pro	Gln	Ala	Arg 445	Tyr	Gln	Arg	Val	Ala 450
Val	His	Arg	Val	Pro 455	Gly	Leu	His	His	Thr 460	Tyr	Asp	Val	Leu	Phe 465
Leu	Gly	Thr	Gly	Asp 470	Gly	Arg	Leu	His	Lys 475	Ala	Val	Ser	Val	Gly 480
Pro	Arg	Val	His	Ile 485	Ile	Glu	Glu	Leu	Gln 490	Ile	Phe	Ser	Ser	Gly 495
Gln	Pro	Val	Gln	Asn 500	Leu	Leu	Leu	Asp	Thr 505	His	Arg	Gly	Leu	Leu 510
Tyr	Ala	Ala	Ser	His 515	Ser	Gly	Val	Val	Gln 520	Val	Pro	Met	Ala	Asn 525
Cys	Ser	Leu	Tyr	Arg 530	Ser	Cys	Gly	Asp	Cys 535	Leu	Leu	Ala	Arg	Asp 540
Pro	Tyr	Cys	Ala	Trp 545	Ser	Gly	Ser	Ser	Cys 550	Lys	His	Val	Ser	Leu 555
Tyr	Gln	Pro	Gln	Leu 560	Ala	Thr	Arg	Pro	Trp 565	Ile	Gln	Asp	Ile	Glu 570
Gly	Ala	Ser	Ala	Lys 575	Asp	Leu	Cys	Ser	Ala 580	Ser	Ser	Val	Val	Ser 585
Pro	Ser	Phe	Val	Pro 590	Thr	Gly	Glu	Lys	Pro 595	Cys	Glu	Gln	Val	Gln 600
Phe	Gln	Pro	Asn	Thr 605	Val	Asn	Thr	Leu	Ala 610	Cys	Pro	Leu	Leu	Ser 615
Asn	Leu	Ala	Thr	Arg 620	Leu	Trp	Leu	Arg	Asn 625	Gly	Ala	Pro	Val	Asn 630
Ala	Ser	Ala	Ser	Cys 635	His	Val	Leu	Pro	Thr 640	Gly	Asp	Leu	Leu	Leu 645
Val	Gly	Thr	Gln	Gln 650	Leu	Gly	Glu	Phe	Gln 655	Cys	Trp	Ser	Leu	Glu 660
Glu	Gly	Phe	Gln	Gln	Leu	Val	Ala	Ser	Tyr	Cys	Pro	Glu	Val	Val

665	670	675
Glu Asp Gly Val Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val Pro	
680	685	690
Val Ile Ile Ser Thr Ser Arg Val Ser	Ala Pro Ala Gly Gly Lys	
695	700	705
Ala Ser Trp Gly Ala Asp Arg Ser Tyr	Trp Lys Glu Phe Leu Val	
710	715	720
Met Cys Thr Leu Phe Val Leu Ala Val	Leu Leu Pro Val Leu Phe	
725	730	735
Leu Leu Tyr Arg His Arg Asn Ser Met	Lys Val Phe Leu Lys Gln	
740	745	750
Gly Glu Cys Ala Ser Val His Pro Lys	Thr Cys Pro Val Val Leu	
755	760	765
Pro Pro Glu Thr Arg Pro Leu Asn Gly	Leu Gly Pro Pro Ser Thr	
770	775	780
Pro Leu Asp His Arg Gly Tyr Gln Ser	Leu Ser Asp Ser Pro Pro	
785	790	795
Gly Ala Arg Val Phe Thr Glu Ser Glu	Lys Arg Pro Leu Ser Ile	
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Gln Asp Ser Phe Val Glu Val Ser Pro	Val Cys Pro Arg Pro Arg	
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Val Arg Leu Gly Ser Glu Ile Arg Asp	Ser Val Val	
830	835	

<210> 254
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 254
 agcccgtagca gaatctgctc ctgg 24

<210> 255
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

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<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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Leu	Val	Leu	Gly	Phe	Val	Leu	Ala	Ser	Arg	Leu	Val	Leu	Pro	Arg	
				20					25					30	
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro	
				35					40					45	
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly	
				50					55					60	
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser	
				65					70					75	
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly	
				80					85					90	
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala	
				95					100					105	
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe	
				110					115					120	
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro	
				125					130					135	
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe	
				140					145					150	
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu	
				155					160					165	
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg	
				170					175					180	
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe	
				185					190					195	
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu	
				200					205					210	
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val	
				215					220					225	
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly	
				230					235					240	

Lys Cys Leu Arg	Glu Met Tyr Thr Thr	His Glu Asp Val Glu Val	245	250	255
Gly Arg Cys Val	Arg Arg Phe Ala Gly	Val Gln Cys Val Trp Ser	260	265	270
Tyr Glu Met Arg	Gln Leu Phe Tyr Glu	Asn Tyr Glu Gln Asn Lys	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln Ala	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg Leu	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His Arg	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr Ser	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro Pro	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu Glu	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp Gly	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala Leu	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn Ala	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr Gly	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu Asp	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr Val	455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys Ile	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala Lys	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn Ser	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser Glu	515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile	Asn Ile Leu Ile Pro Leu			

530										535					540				
Ser	Gly	Arg	Phe	Asp	Met	Phe	Val	Arg		Phe	Met	Gly	Asn	Phe	Glu				
				545						550					555				
Lys	Thr	Cys	Leu	Ile	Pro	Asn	Gln	Asn		Val	Lys	Leu	Val	Val	Leu				
				560						565					570				
Leu	Phe	Asn	Ser	Asp	Ser	Asn	Pro	Asp		Lys	Ala	Lys	Gln	Val	Glu				
				575						580					585				
Leu	Met	Arg	Asp	Tyr	Arg	Ile	Lys	Tyr		Pro	Lys	Ala	Asp	Met	Gln				
				590						595					600				
Ile	Leu	Pro	Val	Ser	Gly	Glu	Phe	Ser		Arg	Ala	Leu	Ala	Leu	Glu				
				605						610					615				
Val	Gly	Ser	Ser	Gln	Phe	Asn	Asn	Glu		Ser	Leu	Leu	Phe	Phe	Cys				
				620						625					630				
Asp	Val	Asp	Leu	Val	Phe	Thr	Thr	Glu		Phe	Leu	Gln	Arg	Cys	Arg				
				635						640					645				
Ala	Asn	Thr	Val	Leu	Gly	Gln	Gln	Ile		Tyr	Phe	Pro	Ile	Ile	Phe				
				650						655					660				
Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr		Ser	Gly	Lys	Val	Pro	Ser				
				665						670					675				
Asp	Asn	His	Phe	Ala	Phe	Thr	Gln	Lys		Thr	Gly	Phe	Trp	Arg	Asn				
				680						685					690				
Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr		Lys	Gly	Asp	Leu	Val	Arg				
				695						700					705				
Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln		Gly	Trp	Gly	Leu	Glu	Asp				
				710						715					720				
Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln		Ala	Gly	Leu	Lys	Thr	Phe				
				725						730					735				
Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His		Val	His	His	Pro	Val	Phe				
				740						745					750				
Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln		Tyr	Lys	Met	Cys	Leu	Gly				
				755						760					765				
Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr		Gln	Gln	Leu	Ala	Glu	Met				
				770						775					780				
Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr		Ser	Lys	Ser	Ser	Asn	Asn				
				785						790					795				
Asn	Gly	Ser	Val	Arg	Thr	Ala													
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<210> 261
 <211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
tcccatttct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45

Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Pro Lys His Val Tyr Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys		
65	70	75
Glu Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu		
80	85	90
Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly		
95	100	105
Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro		
110	115	120
Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala		
125	130	135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu		
140	145	150
Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val		
155	160	165
Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro		
170	175	180
Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu		
185	190	195
Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys		
200	205	210
Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp		
215	220	225
Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala		
230	235	240
Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu		
245	250	255
Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala		
260	265	270
Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro		
275	280	285
Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile		
290	295	300
Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp		
305	310	315
Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val		
320	325	330
Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala		
335	340	345

Leu Leu Lys Val Tyr
350

<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

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<210> 267
 <211> 466
 <212> PRT
 <213> Homo sapiens

<400> 267
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35	40	45
Thr Ser Ala Glu Ala Met Glu Val Arg Phe Phe Arg Asn Gln Phe		
50	55	60
His Ala Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser		
65	70	75
Lys Gln Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp		
80	85	90
Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr		
95	100	105
Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile		
110	115	120
Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly		
125	130	135
Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile		
140	145	150
Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala		
155	160	165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg		
170	175	180
Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile		
185	190	195
Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu		
200	205	210
Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu		
215	220	225
Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu		
230	235	240
Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile		
245	250	255
Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp		
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys		
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys		
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro		
305	310	315

Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val
320 325 330

Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val
335 340 345

Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp
350 355 360

Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn
365 370 375

Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr
380 385 390

Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr
395 400 405

Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe
410 415 420

Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys
425 430 435

Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr
440 445 450

Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp
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Gly

<210> 268
<211> 2103
<212> DNA
<213> Homo sapiens

<400> 268
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gtcatcttca tatccctgat tgtcctggca gtgtgcattg gactcactgt 150
tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
tgtcattttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
atattataaa tctccattaa gggaagaatt tgtcaagtct caggttatca 350
agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400
agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450
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ctaaaccatt	gctgcggaac	acgaagaagt	aaaactctag	gtcagagtct	600
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gccacatggc	ttgtgagtgc	tgctcactgt	tttacaacat	ataagaaccc	750
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aacgggggtct	ccggagaata	attgtccatg	aaaaatacaa	acacccatca	850
catgactatg	atattttctct	tgcagagctt	tctagccctg	ttccctacac	900
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cagaattttg	acttgttgac	ataaatttgt	aatgcatata	tacaatttga	1650
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aatattagaa	atgatcatat	tcattatgaa	aggtcaagca	aagacagcag	1850
aataccaatc	acttcatcat	ttaggaagta	tgggaactaa	gttaaggaag	1900
tccagaaaaga	agccaagata	tatccttatt	ttcattttcca	aacaactact	1950

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 caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat 2050
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 cca 2103

<210> 269
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 269
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 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
 35 40 45
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
 50 55 60
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
 65 70 75
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
 80 85 90
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
 95 100 105
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
 110 115 120
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
 125 130 135
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
 140 145 150
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
 155 160 165
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
 170 175 180
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
 185 190 195
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
 200 205 210
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
 215 220 225

Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro
				230					235					240
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys
				245					250					255
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys
				260					265					270
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser
				275					280					285
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp
				290					295					300
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly
				305					310					315
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg
				320					325					330
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro
				335					340					345
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly
				350					355					360
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly
				365					370					375
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly
				380					385					390
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly
				395					400					405
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys
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Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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ttcccagagc tcagcccttg gccctcaag actttgaaga agaggaggca 250

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cgaccactgc	cgacacctgc	aggtgccctg	caaggagcta	cagagggtcg	350
ggccggcggc	ctgcctgtgc	ccaggactct	ccagccccgc	ccagccgccc	400
gacccgccgc	gcatgggaga	agtgcgcatt	gcggccgaag	agggccgcgc	450
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gccacggcgg	agtcatgggt	ctcaggactg	agcgcttggt	taggtccggt	1050
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<210> 271
<211> 238
<212> PRT
<213> Homo sapiens
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<400> 271														
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				20					25					30
Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
				35					40					45
Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys
				50					55					60
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly
				65					70					75

Leu Ser Ser Pro Ala Gln Pro Pro Asp Pro Pro Arg Met Gly Glu
80 85 90

Val Arg Ile Ala Ala Glu Glu Gly Arg Ala Val Val His Trp Cys
95 100 105

Ala Pro Phe Ser Pro Val Leu His Tyr Trp Leu Leu Leu Trp Asp
110 115 120

Gly Ser Glu Ala Ala Gln Lys Gly Pro Pro Leu Asn Ala Thr Val
125 130 135

Arg Arg Ala Glu Leu Lys Gly Leu Lys Pro Gly Gly Ile Tyr Val
140 145 150

Val Cys Val Val Ala Ala Asn Glu Ala Gly Ala Ser Arg Val Pro
155 160 165

Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp Ile Pro Ala Phe
170 175 180

Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro Arg Thr Leu
185 190 195

Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu Leu Ser
200 205 210

Cys Ala Ala Leu Val Trp His Phe Cys Leu Arg Asp Arg Trp Gly
215 220 225

Cys Pro Arg Arg Ala Ala Ala Arg Ala Ala Gly Ala Leu
230 235

<210> 272
<211> 2397
<212> DNA
<213> Homo sapiens

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 ttctttttct ccagaaaaat gcttgtgaga atcattaaaa catgtgacaa 2200
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<210> 273
 <211> 305
 <212> PRT
 <213> Homo sapiens

<400> 273
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 20 25 30
 Val Ser Ala Trp Met Arg Asp Tyr Leu Asn Asn Val Leu Thr Leu
 35 40 45
 Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe
 50 55 60
 Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile
 65 70 75
 Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu
 80 85 90
 Leu Leu Leu Ala Trp Tyr Phe Gly Ser Leu Leu Val Ile Phe Cys
 95 100 105
 Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met
 110 115 120
 Val Pro Val Gln Trp Ser Asp Met Val Thr Leu Lys Ala Arg Met
 125 130 135
 Thr Asn Tyr Gly Leu Pro Arg Tyr Arg Trp Leu Thr His Ala Trp
 140 145 150
 Asn Phe Phe Gln Arg Glu Phe Lys Cys Cys Gly Val Val Tyr Phe
 155 160 165
 Thr Asp Trp Leu Glu Met Thr Glu Met Asp Trp Pro Pro Asp Ser

170								175							180	
Cys	Cys	Val	Arg	Glu 185	Phe	Pro	Gly	Cys	Ser 190	Lys	Gln	Ala	His	Gln 195		
Glu	Asp	Leu	Ser	Asp 200	Leu	Tyr	Gln	Glu	Gly 205	Cys	Gly	Lys	Lys	Met 210		
Tyr	Ser	Phe	Leu	Arg 215	Gly	Thr	Lys	Gln	Leu 220	Gln	Val	Leu	Arg	Phe 225		
Leu	Gly	Ile	Ser	Ile 230	Gly	Val	Thr	Gln	Ile 235	Leu	Ala	Met	Ile	Leu 240		
Thr	Ile	Thr	Leu	Leu 245	Trp	Ala	Leu	Tyr	Tyr 250	Asp	Arg	Arg	Glu	Pro 255		
Gly	Thr	Asp	Gln	Met 260	Met	Ser	Leu	Lys	Asn 265	Asp	Asn	Ser	Gln	His 270		
Leu	Ser	Cys	Pro	Ser 275	Val	Glu	Leu	Leu	Lys 280	Pro	Ser	Leu	Ser	Arg 285		
Ile	Phe	Glu	His	Thr 290	Ser	Met	Ala	Asn	Ser 295	Phe	Asn	Thr	His	Phe 300		
Glu	Met	Glu	Glu	Leu 305												

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<210> 274
<211> 2063
<212> DNA
<213> Homo sapiens
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cttgggggtga	caatctcagc	tccaggctac	agggagaccg	ggaggatcac	200
agagccagca	tgttacagga	tcctgacagt	gatcaacctc	tgaacagcct	250
cgatgtcaaa	cccctgcgca	aaccccgtat	ccccatggag	accttcagaa	300
aggtggggat	ccccatcatc	atagcactac	tgagcctggc	gagtatcatc	350
attgtggttg	tcctcatcaa	ggtgattctg	gataaatact	acttcctctg	400
cgggcagcct	ctccacttca	tcccaggaa	gcagctgtgt	gacggagagc	450
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gaagggcctg	cagtggcagt	ccgcctctcc	aaggaccgat	ccacactgca	550
ggtgctggac	tcggccacag	ggaactggtt	ctctgcctgt	ttcgacaact	600

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 aaacagccag gagcttcgca tgcggaactc aagtggggccc tgtctctcag 750
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<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp
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Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg
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Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser
35 40 45

Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr
50 55 60

Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
65 70 75

Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu
80 85 90

His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg
95 100 105

Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr
110 115 120

Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu
125 130 135

Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu
140 145 150

Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn
155 160 165

Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser
170 175 180

Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu
185 190 195

Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser
200 205 210

Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys
215 220 225

Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His
230 235 240

Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala
245 250 255

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<210> 277
<211> 761
<212> PRT
<213> Homo sapiens
<400> 277
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Ala Gly Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr
35 40 45

Ala Gly Asp Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly
50 55 60

Leu Gln Asp Phe Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr
65 70 75

Leu Tyr Val Gly Ala Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln
80 85 90

Asp Pro Gly Val Pro Arg Leu Lys Asn Met Ile Pro Trp Pro Ala
95 100 105

Ser Asp Arg Lys Lys Ser Glu Cys Ala Phe Lys Lys Lys Ser Asn
110 115 120

Glu Thr Gln Cys Phe Asn Phe Ile Arg Val Leu Val Ser Tyr Asn
125 130 135

Val Thr His Leu Tyr Thr Cys Gly Thr Phe Ala Phe Ser Pro Ala
140 145 150

Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr Leu Leu Pro Ile Ser
155 160 165

Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser Pro Phe Asp Pro
170 175 180

Ala His Lys His Thr Ala Val Leu Val Asp Gly Met Leu Tyr Ser
185 190 195

Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu Met Arg
200 205 210

Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu Arg
215 220 225

Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr
230 235 240

Gln Val Val Tyr Phe Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp
245 250 255

Phe Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys
260 265 270

Asn Asp Val Gly Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr
275 280 285

Phe Leu Lys Ala Gln Leu Leu Cys Thr Gln Pro Gly Gln Leu Pro

270

Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu
590 595 600

Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln
605 610 615

Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly
620 625 630

Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln
635 640 645

Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His
650 655 660

Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala
665 670 675

Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu
680 685 690

Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser
695 700 705

Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu
710 715 720

Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His
725 730 735

Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp
740 745 750

Ala Asp Asn Asn Cys Leu Gly Thr Glu Val Ala
755 760

<210> 278
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 278
ctgctggtga aatctggcgt ggag 24

<210> 279
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

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<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282

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Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
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Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile
				155					160					165
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro
				170					175					180
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met
				185					190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe
				200					205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile
				215					220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu
				230					235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe
				245					250					255
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly

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Leu Met Glu Lys Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu Asn	
275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu	
290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys Glu	
305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys	
320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp	Val His Leu Ala Ala Asn	
335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His	
350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile	
365	370	375
Met Glu Ala Ile Gln His Gly Val Pro	Met Val Gly Ile Pro Leu	
380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys	
395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu	
410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser	
425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser	
440	445	450
Pro Thr Gln Arg Leu Val Gly Trp Ile	Asp His Val Leu Gln Thr	
455	460	465
Gly Gly Ala Thr His Leu Lys Pro Tyr	Val Phe Gln Gln Pro Trp	
470	475	480
His Glu Gln Tyr Leu Phe Asp Val Phe	Val Phe Leu Leu Gly Leu	
485	490	495
Thr Leu Gly Thr Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met Ala	
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Val Trp Trp Leu Arg Gly Ala Arg Lys	Val Lys Glu Thr	
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<210> 283
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 283
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<210> 284
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 284
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<210> 285
 <211> 45
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-45
 <223> Synthetic construct.

<400> 285
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<210> 286
 <211> 2340
 <212> DNA
 <213> Homo sapiens

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<210> 287
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 287
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 20 25 30
 Trp Ala Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys
 35 40 45
 Leu Val Val Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly
 50 55 60
 Gly Ala Ala Leu Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Ala
 65 70 75
 Ala Val Arg Ser His His His Glu Pro Ala Gly Glu Thr Gly Asn
 80 85 90
 Gly Thr Ser Gly Ala Ile Tyr Phe Asp Gln Val Leu Val Asn Glu
 95 100 105
 Gly Gly Gly Phe Asp Arg Ala Ser Gly Ser Phe Val Ala Pro Val
 110 115 120
 Arg Gly Val Tyr Ser Phe Arg Phe His Val Val Lys Val Tyr Asn
 125 130 135
 Arg Gln Thr Val Gln Val Ser Leu Met Leu Asn Thr Trp Pro Val
 140 145 150
 Ile Ser Ala Phe Ala Asn Asp Pro Asp Val Thr Arg Glu Ala Ala
 155 160 165
 Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly Asp Arg Val Ser

170

175

180

Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser
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Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu
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<210> 288
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 288
 aggcagccac cagctctgtg ctac 24

<210> 289
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

<400> 289
 cagagaggga agatgaggaa gccagag 27

<210> 290
 <211> 42
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-42
 <223> Synthetic construct.

<400> 290
 ctgtgctact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291
 <211> 1570
 <212> DNA
 <213> Homo sapiens

<400> 291
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ttccccgctgg gccgtgactg ggcgggcttc agccatgaag accctcatag 200
 ccgcctactc cggggctcctg cgcggcgagc gtcaggccga ggctgaccgg 250
 agccagcgct ctcacggagg acctgcgctg tcgcgcgagg ggtctgggag 300
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<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292

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Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser	35	40	45	
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn	50	55	60	
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln	65	70	75	
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile	80	85	90	
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu	95	100	105	
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly	110	115	120	
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr	125	130	135	
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu	140	145	150	
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile	155	160	165	
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu	170	175	180	
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu	185	190	195	
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser	200	205	210	
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu	215	220	225	
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly	230	235	240	
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr	245	250	255	
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly				

260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe	Gly Glu Asn Glu Val Tyr	
275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser	Trp Gly Arg Trp Val Gln	
290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe	Ala Pro Cys Ile Phe His	
305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr	Trp Gly Leu Val Pro Tyr	
320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly	Glu Pro Ile Thr Ile Pro	
335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp	Ile Asp Leu Tyr His Thr	
350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu	Phe Asp Lys His Lys Thr	
365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val	Leu Glu Val Asn	
380	385	

<210> 293
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 293
 gctgacctgg ttcccatcta ctcc 24

<210> 294
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 294
 cccacagaca cccatgacac ttcc 24

<210> 295
 <211> 50
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 295
 aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296
 <211> 3060
 <212> DNA
 <213> Homo sapiens

<400> 296
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 cggggccgcg gaggcgacgc cggggacgcc cgcgcgacga gcagggtggc 150
 gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200
 ggctctgctg accttgtgcc ttggacggct gtctcagcg agggggccgtg 250
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aaaaacccca	gaaattcttg	agttgaaactg	tgtagttact	gacatgaaaa	1500
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cctttttaaa	tttttattat	ttattttatt	atctattttt	agacagggtc	2600

Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe	
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Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys	
				185					190					195	
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	
				200					205					210	
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val	
				215					220					225	
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu	
				230					235					240	
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	
				245					250					255	
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala	
				260					265					270	
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	
				275					280					285	
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys	
				290					295					300	
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala	
				305					310					315	
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	
				320					325					330	
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	
				335					340					345	
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu	
				350					355					360	
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln								
				365											

<210> 298

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 298

cttcctctgt gggtggacca tgtg 24

<210> 299

<211> 21

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

gccacctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggtcct cgctaagaag gagctgctct acgtgccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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 tcagtttgtc ttgtgggggtt ggtggcaggc aggccggctt acgcctgata 200
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<210> 302
<211> 143
<212> PRT
<213> Homo sapiens
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<400> 302

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His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
				20					25					30
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35					40					45
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50					55					60
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
				65					70					75
Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr
				80					85					90
Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln
				95					100					105
Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu
				110					115					120
Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr
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Cys	Gly	Val	Leu	Leu	Ser	Phe	Leu							

140

<210> 303
 <211> 1768
 <212> DNA
 <213> Homo sapiens

<400> 303
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 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700
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<210> 304
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 304
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 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly
 35 40 45
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
 50 55 60
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro
 65 70 75
 Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala
 80 85 90
 Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly
 95 100 105
 Arg Arg Arg Asp

<210> 305
 <211> 989
 <212> DNA
 <213> Homo sapiens

<400> 305

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<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

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				20					25					30
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
				35					40					45
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
				50					55					60

Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu
65 70 75

Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln
80 85 90

Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys
95 100 105

Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu
110 115 120

Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val
125 130 135

Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala
140 145 150

Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu
155 160 165

Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp
170 175 180

Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr
185 190 195

Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly Gly Ile Leu Ala Val
200 205 210

Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln Pro Pro Lys Gly
215 220 225

Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg
230 235 240

Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly
245 250 255

Leu Thr Leu Ala Phe Lys Ile
260

<210> 307
<211> 2272
<212> DNA
<213> Homo sapiens

<400> 307
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ggatggcgcc gtgaagcccc cacccaacaa gtaccccatc tttttctttg 200
gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250

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aaggtgtggc tcctctgaag acctgcacga cagcgtacgg gaggggtccc 2000
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<210> 308
<211> 671
<212> PRT
<213> Homo sapiens

<400> 308
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20 25 30
Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe
35 40 45
Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro
50 55 60
Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys
65 70 75
Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala
80 85 90
Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala
95 100 105
Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp
110 115 120
Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala
125 130 135
Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser

140										145					150				
Asp	Asn	Ser	Gly	Leu	Lys	Arg	Lys	Thr	Pro	Ala	Leu	Lys	Met	Ser					
				155					160					165					
Val	Ser	Lys	Arg	Ala	Arg	Lys	Ala	Ser	Ser	Asp	Leu	Asp	Gln	Ala					
				170					175					180					
Ser	Val	Ser	Pro	Ser	Glu	Glu	Glu	Asn	Ser	Glu	Ser	Ser	Ser	Glu					
				185					190					195					
Ser	Glu	Lys	Thr	Ser	Asp	Gln	Asp	Phe	Thr	Pro	Glu	Lys	Lys	Ala					
				200					205					210					
Ala	Val	Arg	Ala	Pro	Arg	Arg	Gly	Pro	Leu	Gly	Gly	Arg	Lys	Lys					
				215					220					225					
Lys	Lys	Ala	Pro	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Lys	Ala	Asp	Ser					
				230					235					240					
Asp	Gly	Ala	Lys	Pro	Glu	Pro	Val	Ala	Met	Ala	Arg	Ser	Ala	Ser					
				245					250					255					
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Asp	Val	Ser	Val					
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Lys	Lys	Pro	Pro	Arg	Gly	Arg	Lys	Pro	Ala	Glu	Lys	Pro	Leu	Pro					
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Lys	Pro	Arg	Gly	Arg	Lys	Pro	Lys	Pro	Glu	Arg	Pro	Pro	Ser	Ser					
				290					295					300					
Ser	Ser	Ser	Asp	Ser	Asp	Ser	Asp	Glu	Val	Asp	Arg	Ile	Ser	Glu					
				305					310					315					
Trp	Lys	Arg	Arg	Asp	Glu	Ala	Arg	Arg	Arg	Glu	Leu	Glu	Ala	Arg					
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Glu	Lys	Glu	Glu	Lys	Glu	Arg	Arg	Arg	Glu	Arg	Ala	Asp	Arg	Gly					
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Glu	Ala	Glu	Arg	Gly	Ser	Gly	Gly	Ser	Ser	Gly	Asp	Glu	Leu	Arg					
				365					370					375					
Glu	Asp	Asp	Glu	Pro	Val	Lys	Lys	Arg	Gly	Arg	Lys	Gly	Arg	Gly					
				380					385					390					
Arg	Gly	Pro	Pro	Ser	Ser	Ser	Asp	Ser	Glu	Pro	Glu	Ala	Glu	Leu					
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Glu	Arg	Glu	Ala	Lys	Lys	Ser	Ala	Lys	Lys	Pro	Gln	Ser	Ser	Ser					
				410					415					420					
Thr	Glu	Pro	Ala	Arg	Lys	Pro	Gly	Gln	Lys	Glu	Lys	Arg	Val	Arg					
				425					430					435					

Pro	Glu	Glu	Lys	Gln	Gln	Ala	Lys	Pro	Val	Lys	Val	Glu	Arg	Thr	440	445	450
Arg	Lys	Arg	Ser	Glu	Gly	Phe	Ser	Met	Asp	Arg	Lys	Val	Glu	Lys	455	460	465
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Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg	485	490	495
Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser	500	505	510
Gln	Ile	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala	Thr	Leu	Lys	Lys	515	520	525
Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala	Ala	530	535	540
Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro	Lys	Ile	545	550	555
Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys	560	565	570
Ala	Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala	575	580	585
Pro	Gln	Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala	590	595	600
Pro	Val	Asn	Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu	605	610	615
Asp	Lys	Glu	His	Glu	Glu	Gly	Arg	Asp	Ser	Glu	Glu	Gly	Pro	Arg	620	625	630
Cys	Gly	Ser	Ser	Glu	Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro	635	640	645
Asp	Leu	Asp	Arg	Pro	Gly	Ser	Asp	Arg	Gln	Glu	Arg	Glu	Arg	Ala	650	655	660
Arg	Gly	Asp	Ser	Glu	Ala	Leu	Asp	Glu	Glu	Ser					665	670	

<210> 309

<211> 3871

<212> DNA

<213> Homo sapiens

<400> 309

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$\langle 210 \rangle$ 310

<211> 777

<212> PRT

<213> Homo sapiens

$\langle 400 \rangle$ 310

Met Asn Ala Asn Lys Asp Glu Arg Leu Lys Ala Arg Ser Gln Asp
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Phe His Leu Phe Pro Ala Leu Met Met Leu Ser Met Thr Met Leu
20 25 30

Phe Leu Pro Val Thr Gly Thr Leu Lys Gln Asn Ile Pro Arg Leu
35 40 45

Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro
50 55 60

Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu
65 70 75

Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

80										85					90				
Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile					
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Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala					
				110					115					120					
Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu					
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Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala					
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Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu					
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Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg					
				170					175					180					
Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met					
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Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly					
				200					205					210					
Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His					
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His	Tyr	Ile	Arg	Thr	Asp	Ile	Ser	Glu	His	Tyr	Trp	Leu	Asn	Gly					
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Ala	Lys	Phe	Ile	Gly	Thr	Phe	Phe	Ile	Pro	Asp	Thr	Tyr	Asn	Pro					
				245					250					255					
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Arg	Glu	Ser	Ser	Gln	Glu					
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Gly	Ser	Thr	Ser	Asp	Lys	Thr	Ile	Leu	Ser	Arg	Val	Gly	Arg	Val					
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Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Trp					
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Thr	Thr	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	Ser	Ile	Pro	Gly	Ser					
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Asp	Gly	Ala	Asp	Thr	Tyr	Phe	Asp	Glu	Leu	Gln	Asp	Ile	Tyr	Leu					
				320					325					330					
Leu	Pro	Thr	Arg	Asp	Glu	Arg	Asn	Pro	Val	Val	Tyr	Gly	Val	Phe					
				335					340					345					
Thr	Thr	Thr	Ser	Ser	Ile	Phe	Lys	Gly	Ser	Ala	Val	Cys	Val	Tyr					
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Ser	Met	Ala	Asp	Ile	Arg	Ala	Val	Phe	Asn	Gly	Pro	Tyr	Ala	His					
				365					370					375					

Lys Glu Ser Ala Asp His Arg Trp Val Gln Tyr Asp Gly Arg Ile
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 Pro Tyr Pro Arg Pro Gly Thr Cys Pro Ser Lys Thr Tyr Asp Pro
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 Leu Ile Lys Ser Thr Arg Asp Phe Pro Asp Asp Val Ile Ser Phe
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 Ile Lys Arg His Ser Val Met Tyr Lys Ser Val Tyr Pro Val Ala
 425 430 435
 Gly Gly Pro Thr Phe Lys Arg Ile Asn Val Asp Tyr Arg Leu Thr
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 Gln Ile Val Val Asp His Val Ile Ala Glu Asp Gly Gln Tyr Asp
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 Val Met Phe Leu Gly Thr Asp Ile Gly Thr Val Leu Lys Val Val
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 Ser Ile Ser Lys Glu Lys Trp Asn Met Glu Glu Val Val Leu Glu
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 Glu Leu Gln Ile Phe Lys His Ser Ser Ile Ile Leu Asn Met Glu
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 Leu Ser Leu Lys Gln Gln Gln Leu Tyr Ile Gly Ser Arg Asp Gly
 515 520 525
 Leu Val Gln Leu Ser Leu His Arg Cys Asp Thr Tyr Gly Lys Ala
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 Cys Ala Asp Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp
 545 550 555
 Gly Asn Ala Cys Ser Arg Tyr Ala Pro Thr Ser Lys Arg Arg Ala
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 Arg Arg Gln Asp Val Lys Tyr Gly Asp Pro Ile Thr Gln Cys Trp
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 Asp Ile Glu Asp Ser Ile Ser His Glu Thr Ala Asp Glu Lys Val
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 Ile Phe Gly Ile Glu Phe Asn Ser Thr Phe Leu Glu Cys Ile Pro
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 Lys Ser Gln Gln Ala Thr Ile Lys Trp Tyr Ile Gln Arg Ser Gly
 620 625 630
 Asp Glu His Arg Glu Glu Leu Lys Pro Asp Glu Arg Ile Ile Lys
 635 640 645
 Thr Glu Tyr Gly Leu Leu Ile Arg Ser Leu Gln Lys Lys Asp Ser
 650 655 660
 Gly Met Tyr Tyr Cys Lys Ala Gln Glu His Thr Phe Ile His Thr

665	670	675
Ile Val Lys Leu Thr Leu Asn Val Ile	Glu Asn Glu Gln Met Glu	
680	685	690
Asn Thr Gln Arg Ala Glu His Glu Glu	Gly Gln Val Lys Asp Leu	
695	700	705
Leu Ala Glu Ser Arg Leu Arg Tyr Lys	Asp Tyr Ile Gln Ile Leu	
710	715	720
Ser Ser Pro Asn Phe Ser Leu Asp Gln	Tyr Cys Glu Gln Met Trp	
725	730	735
His Arg Glu Lys Arg Arg Gln Arg Asn	Lys Gly Gly Pro Lys Trp	
740	745	750
Lys His Met Gln Glu Met Lys Lys Lys	Arg Asn Arg Arg His His	
755	760	765
Arg Asp Leu Asp Glu Leu Pro Arg Ala	Val Ala Thr	
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 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 311
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<210> 312
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 312
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<210> 313
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 313
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<210> 314
<211> 3934
<212> DNA
<213> Homo sapiens

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<210> 315
 <211> 370
 <212> PRT
 <213> Homo sapiens

<400> 315
 Met Gln Leu Ala Lys Tyr Gln Ser His Ser Lys Ser Cys Pro Thr
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Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu	20	25	30
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala	35	40	45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg	50	55	60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu	65	70	75
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala	80	85	90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser	95	100	105
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp	110	115	120
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu	125	130	135
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro	140	145	150
Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp	155	160	165
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu	170	175	180
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu	185	190	195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser	200	205	210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu	215	220	225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln	230	235	240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu	245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly	260	265	270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu	275	280	285
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu	290	295	300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala			

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<210> 317
<211> 837
<212> PRT
<213> Homo sapiens

<400> 317

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Trp	Leu	Trp	Gly	Ala	Gln	Pro	Cys	Leu	Leu	Leu	Pro	Ile	Val	Pro	20	25	30	
Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu	35	40	45		
Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu	50	55	60	
Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser	65	70	75	
Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu	80	85	90	
Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu	95	100	105	
Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly	110	115	120	
Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp	125	130	135	
Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu				

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Gly Val Leu Gln Tyr Arg Gly Ala Glu	Leu His Leu Gln Pro	Leu
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Glu Gly Gly Thr Pro Asn Ser Ala Gly	Gly Pro Gly Ala His	Ile
170	175	180
Leu Arg Arg Lys Ser Pro Ala Ser Gly	Gln Gly Pro Met Cys	Asn
185	190	195
Val Lys Ala Pro Leu Gly Ser Pro Ser	Pro Arg Pro Arg Arg	Ala
200	205	210
Lys Arg Phe Ala Ser Leu Ser Arg Phe	Val Glu Thr Leu Val	Val
215	220	225
Ala Asp Asp Lys Met Ala Ala Phe His	Gly Ala Gly Leu Lys	Arg
230	235	240
Tyr Leu Leu Thr Val Met Ala Ala Ala	Ala Lys Ala Phe Lys	His
245	250	255
Pro Ser Ile Arg Asn Pro Val Ser Leu	Val Val Thr Arg Leu	Val
260	265	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro	Gln Val Gly Pro Ser	Ala
275	280	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala	Trp Gln Arg Gly Leu	Asn
290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His	Phe Asp Thr Ala Ile	Leu
305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val	Ser Thr Cys Asp Thr	Leu
320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys	Asp Pro Ala Arg Ser	Cys
335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln	Ser Ala Phe Thr Ala	Ala
350	355	360
His Glu Leu Gly His Val Phe Asn Met	Leu His Asp Asn Ser	Lys
365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu	Ser Thr Ser Arg His	Val
380	385	390
Met Ala Pro Val Met Ala His Val Asp	Pro Glu Glu Pro Trp	Ser
395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp	Phe Leu Asp Asn Gly	Tyr
410	415	420
Gly His Cys Leu Leu Asp Lys Pro Glu	Ala Pro Leu His Leu	Pro
425	430	435

Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln	440	445	450
Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro	455	460	465
Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala	470	475	480
Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys	485	490	495
Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp	500	505	510
Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro	515	520	525
Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val	530	535	540
Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly	545	550	555
Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn	560	565	570
Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu	575	580	585
Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe	590	595	600
Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro	605	610	615
Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr	620	625	630
Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser	635	640	645
Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala	650	655	660
Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys	665	670	675
Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly	680	685	690
Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile	695	700	705
Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro	710	715	720
Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser			

725	730	735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp		
740	745	750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr		
755	760	765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro		
770	775	780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg		
785	790	795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro		
800	805	810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu		
815	820	825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys		
830	835	

<210> 318
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 318
 ccctgaagct gccagatggc tcc 23

<210> 319
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 319
 ctgtgctctt cggtgcagcc agtc 24

<210> 320
 <211> 43
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-43
 <223> Synthetic construct.

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
305 310 315

Arg Val

<210> 323
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 323
gcggaactgg ctccggctgg cacctgagga gcggcgtgac cccgagggcc 50
cagggagctg cccggctggc ctaggcaggc agccgcacca tggccagcac 100
ggccgtgcag cttctgggct tcctgctcag cttcctgggc atggtgggca 150
cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtgggc 200
accaacatcc tcacggccgt gtcctacctg aaagggctct ggatggagtg 250
tgtgtggcac agcacaggca tctaccagtg ccagatctac cgatccctgc 300
tggcgtgccc ccaagacctc caggctgccc gcgccctcat ggtcatctcc 350
tgctgtctct cgggcatagc ctgcgcctgc gccgtcatcg ggatgaagtg 400
cacgcgtgac gccaaaggga caccgcgcaa gaccaccttt gccatcctcg 450
gcggcaccct cttcatcctg gccggcctcc tgtgcatggt ggccgtctcc 500
tggaccacca acgacgtggt gcagaacttc tacaaccgcg tgctgcccag 550
cgccatgaag tttgagattg gccaggccct gtacctgggc ttcattctct 600
cgtccctctc gtcattggt ggcaccctgc tttgcctgtc ctgccaggac 650
gaggcaccct acaggcccta ccaggccccg cccaggggca ccacgaccac 700
tgcaaaccac gcacctgcct accagccacc agctgcctac aaagacaatc 750
gggccccctc agtgacctcg gccacgcaca gcgggtacag gctgaacgac 800
tacgtgtgag tccccacagc ctgcttctcc cctgggctgc tgtgggctgg 850
gtccccggcg ggactgtcaa tggaggcagg ggttcagca caaagtttac 900
ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaatgt 950
ctttagagca caggacaga gggggaaata agaggaggag aaagctctct 1000

ataccaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050
 atatttatgt gggtgatttg ataacaagtt taatataaag tgacttgga 1100
 gtttggtcag tggggttggt ttgtgatcca ggaataaacc ttgcggatgt 1150
 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe	1	5	10	15
Leu	Gly	Met	Val	Gly	Thr	Leu	Ile	Thr	Thr	Ile	Leu	Pro	His	Trp	20	25	30	
Arg	Arg	Thr	Ala	His	Val	Gly	Thr	Asn	Ile	Leu	Thr	Ala	Val	Ser	35	40	45	
Tyr	Leu	Lys	Gly	Leu	Trp	Met	Glu	Cys	Val	Trp	His	Ser	Thr	Gly	50	55	60	
Ile	Tyr	Gln	Cys	Gln	Ile	Tyr	Arg	Ser	Leu	Leu	Ala	Leu	Pro	Gln	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Met	Val	Ile	Ser	Cys	Leu	Leu	80	85	90	
Ser	Gly	Ile	Ala	Cys	Ala	Cys	Ala	Val	Ile	Gly	Met	Lys	Cys	Thr	95	100	105	
Arg	Cys	Ala	Lys	Gly	Thr	Pro	Ala	Lys	Thr	Thr	Phe	Ala	Ile	Leu	110	115	120	
Gly	Gly	Thr	Leu	Phe	Ile	Leu	Ala	Gly	Leu	Leu	Cys	Met	Val	Ala	125	130	135	
Val	Ser	Trp	Thr	Thr	Asn	Asp	Val	Val	Gln	Asn	Phe	Tyr	Asn	Pro	140	145	150	
Leu	Leu	Pro	Ser	Gly	Met	Lys	Phe	Glu	Ile	Gly	Gln	Ala	Leu	Tyr	155	160	165	
Leu	Gly	Phe	Ile	Ser	Ser	Ser	Leu	Ser	Leu	Ile	Gly	Gly	Thr	Leu	170	175	180	
Leu	Cys	Leu	Ser	Cys	Gln	Asp	Glu	Ala	Pro	Tyr	Arg	Pro	Tyr	Gln	185	190	195	
Ala	Pro	Pro	Arg	Ala	Thr	Thr	Thr	Thr	Ala	Asn	Thr	Ala	Pro	Ala	200	205	210	
Tyr	Gln	Pro	Pro	Ala	Ala	Tyr	Lys	Asp	Asn	Arg	Ala	Pro	Ser	Val	215	220	225	

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
230 235

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<210> 325
<211> 2121
<212> DNA
<213> Homo sapiens
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<400> 325
gagctcccct caggagcgcg ttagcttcac accttcggca gcaggagggc 50
ggcagcttct cgcaggcggc agggcgggcg gccaggatca tgtccaccac 100
cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct 150
gcatcgcggc caccgggatg gacatgtgga gacccagga cctgtacgac 200
aaccctgtca cctccgtggt ccagtacgaa gggctctgga ggagctgcgt 250
gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300
gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcac 350
gtcctgggtg ccattggcct cctggtatcc atctttgcc tgaaatgcat 400
ccgcattggc agcatggagg actctgccaa agccaacatg aactgacct 450
ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct 500
gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaaca 550
gtacaccggc atgggtggga tgggtgcagac tggtcagacc aggtacacat 600
ttggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650
gggggtgtga tgatgtgcat cgcctgccgg ggcctggcac cagaagaaac 700
caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750
agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800
aagaagatat acgatggagg tgcccgaca gaggacgagg tacaatctta 850
tccttccaag cagcactatg tgtaatgtc taagacctct cagcacgggc 900
ggaagaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag 950
atctcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000
catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050
ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100
atcttcaatc ctctatttct ttttttaaata ataactttct actctgatga 1150
gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200
ccccctcttc ctctagtca ataaacccat tgatgatcta tttccagct 1250

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tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300
 ttctgctggt tgaattttgt ctccccaccc ccaacttggc tagtaataaa 1350
 cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400
 cccatgatct cgggttttctt acaactgtgat cttaaaagtt accaaaccaa 1450
 agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct 1500
 tcttattaca gcaacaccat tctaggagtt tctgagctc tccactggag 1550
 tcctctttct gtcgcgggtc agaaattgtc cctagatgaa tgagaaaatt 1600
 atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650
 taaaatgata cactatctct gtgaaatagc ctcacccta catgtggata 1700
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800
 agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950
 gaggctgagg tgggaggatc acttgagccc agggagggtg gggctgcagt 2000
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
 gtctaaaaaa ataaaaaata aataatggaa cacagcaagt cctaggaagt 2100
 aggttaaaac taattcttta a 2121

<210> 326
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 326
 Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile
 1 5 10 15
 Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp
 20 25 30
 Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln
 35 40 45
 Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
 50 55 60
 Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
 65 70 75
 Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

80										85					90				
Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe		Ala	Leu	Lys	Cys	Ile	Arg				
				95						100					105				
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys		Ala	Asn	Met	Thr	Leu	Thr				
				110						115					120				
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly		Leu	Cys	Ala	Ile	Ala	Gly				
				125						130					135				
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val		Thr	Asn	Phe	Trp	Met	Ser				
				140						145					150				
Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly		Gly	Met	Val	Gln	Thr	Val				
				155						160					165				
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala		Leu	Phe	Val	Gly	Trp	Val				
				170						175					180				
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly		Val	Met	Met	Cys	Ile	Ala				
				185						190					195				
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr		Asn	Tyr	Lys	Ala	Val	Ser				
				200						205					210				
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala		Tyr	Lys	Pro	Gly	Gly	Phe				
				215						220					225				
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn		Thr	Lys	Asn	Lys	Lys	Ile				
				230						235					240				
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp		Glu	Val	Gln	Ser	Tyr	Pro				
				245						250					255				
Ser	Lys	His	Asp	Tyr	Val														
				260															

<210> 327
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<400> 327
 ggaaaaactg ttctcttctg tggcacagag aacctgctt caaagcagaa 50
 gtagcagttc cggagtccag ctggctaaaa ctcatcccag aggataatgg 100
 caacccatgc cttagaaatc gctgggctgt ttcttggtgg tgttggaatg 150
 gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgctggcctt 200
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250
 tgaattgcgt gaggcaggct aacatcagga tgcagtgcaa aatctatgat 300
 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350

tgctgcttcc gtgatgtcct tcttggtttt catgatggcc atccttgcca 400
 tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450
 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500
 ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550
 tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga 600
 tggaccacgg cactggtgct gattgttggg ggagctctgt tctgctgctg 650
 tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700
 atcgcacaaac ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750
 tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800
 taaagccatg caaatgacaa aaatctatat tacttttctca aaatggaccc 850
 caaagaaaact ttgatttact gttcttaact gcctaattctt aattacagga 900
 actgtgcatc agctatttat gattctataa gctatttcag cagaatgaga 950
 tattaacccc aatgctttga ttgttctaga aagtatagta atttgttttc 1000
 taaggtgggt caagcatcta ctctttttat catttacttc aaaatgacat 1050
 tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100
 tatgtacata gatgagtgtg acatttatat ctccataga gacatgctta 1150
 tatgggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200
 actcaactat tgcttttcag ggaaatcatg gataggggtg aagaaggtta 1250
 ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat 1300
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350
 tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400
 atcctcttct cccagaggct ttttttttct tgtgtattaa attaacattt 1450
 ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc 1500
 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550
 gtttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650
 gagtacagac tttgagggtt catcaatata aataaaagag cagaaaaata 1700
 tgtcttggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagttgt 1750
 cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800

atttttgttc tgtgaaaaat aaatttcctt cttgtacat ttctgtttag 1850
 ttttactaaa atctgtaaaat actgtatttt tctgtttatt ccaaatttga 1900
 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950
 aatgaatgtg ttctattttgc ttatacatt tatattaata aattgtacat 2000
 ttttctaatt 2010

<210> 328
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 328
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly
 1 5 10 15
 Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp
 20 25 30
 Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn
 35 40 45
 Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile
 50 55 60
 Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro
 65 70 75
 Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met
 80 85 90
 Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu
 110 115 120
 Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile
 125 130 135
 Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn
 140 145 150
 Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu
 155 160 165
 Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala
 170 175 180
 Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr
 185 190 195
 Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
 200 205 210

Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
215 220 225

<210> 329
<211> 1315
<212> DNA
<213> Homo sapiens

<400> 329
tcgcatggc ctctgccga atgcagatcc tgggagtcgt cctgacactg 50
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gaccgctttc atcggcaaca gcatcgtggt ggcccagggtg gtgtgggagg 150
gcctgtggat gtctgcgtg gtgcagagca ccggccagat gcagtgaag 200
gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctggtctacc 300
ttgtctggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350
cgctgtgtgc tcacctctgg gattgtcttt gtcactctcag gggctctgac 400
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gctactcaac atctgcccct gccatctctc gggggccctc tgagtaccct 650
accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700
gagccatcca gaagtggcag tgcccaacag ctttgggatg ggttcgtacc 750
ttttgtttct gcctcctgct atttttcttt tgactgagga tatttaaat 800
tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850
gctgtttctc acccttgat gatggagcca aagaggggat gctttgagat 900
tctggatctt gacatgccc tcttagaagc cagtcaagct atggaactaa 950
tgcgagggt gcttgctgtg ctggctttgc aacaagacag actgtcccca 1000
agagttcctg ctgctgctgg gggctgggct tccctagatg tcaactggaca 1050
gctgcccccc atcctactca ggtctctgga gctcctctct tcaccctgg 1100
aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150
cctctgtttc ctccgtcctg ataagacgtc cccccccag ggccagggtcc 1200
cagctatgta gacccccgcc cccacctcca aactgcacc cttctgcct 1250

gccccctcg tctcaccccc tttaactca catttttatc aaataaagca 1300

tgttttgtta gtgca 1315

<210> 330
<211> 220
<212> PRT
<213> Homo sapiens

<400> 330
Met Ala Ser Ala Gly Met Gln Ile Leu Gly Val Val Leu Thr Leu
1 5 10 15
Leu Gly Trp Val Asn Gly Leu Val Ser Cys Ala Leu Pro Met Trp
20 25 30
Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val
35 40 45
Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly
50 55 60
Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln
65 70 75
Asp Leu Gln Ala Ala Arg Ala Leu Cys Val Ile Ala Leu Leu Val
80 85 90
Ala Leu Phe Gly Leu Leu Val Tyr Leu Ala Gly Ala Lys Cys Thr
95 100 105
Thr Cys Val Glu Glu Lys Asp Ser Lys Ala Arg Leu Val Leu Thr
110 115 120
Ser Gly Ile Val Phe Val Ile Ser Gly Val Leu Thr Leu Ile Pro
125 130 135
Val Cys Trp Thr Ala His Ala Ile Ile Arg Asp Phe Tyr Asn Pro
140 145 150
Leu Val Ala Glu Ala Gln Lys Arg Glu Leu Gly Ala Ser Leu Tyr
155 160 165
Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu Gly Gly Gly Leu
170 175 180
Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly Pro Ser His
185 190 195
Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser Arg Gly
200 205 210
Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
215 220

<210> 331
<211> 1160
<212> DNA

1	5	10	15
Tyr Ser Ser Leu	Leu Ala Leu Pro Pro	Ala Leu Glu Thr Ala Arg	
	20	25	30
Ala Leu Met Cys	Val Ala Val Ala Leu	Ser Leu Ile Ala Leu Leu	
	35	40	45
Ile Gly Ile Cys	Gly Met Lys Gln Val	Gln Cys Thr Gly Ser Asn	
	50	55	60
Glu Arg Ala Lys	Ala Tyr Leu Leu Gly	Thr Ser Gly Val Leu Phe	
	65	70	75
Ile Leu Thr Gly	Ile Phe Val Leu Ile	Pro Val Ser Trp Thr Ala	
	80	85	90
Asn Ile Ile Ile	Arg Asp Phe Tyr Asn	Pro Ala Ile His Ile Gly	
	95	100	105
Gln Lys Arg Glu	Leu Gly Ala Ala Leu	Phe Leu Gly Trp Ala Ser	
	110	115	120
Ala Ala Val Leu	Phe Ile Gly Gly Gly	Leu Leu Cys Gly Phe Cys	
	125	130	135
Cys Cys Asn Arg	Lys Lys Gln Gly Tyr	Arg Tyr Pro Val Pro Gly	
	140	145	150
Tyr Arg Val Pro	His Thr Asp Lys Arg	Arg Asn Thr Thr Met Leu	
	155	160	165
Ser Lys Thr Ser	Thr Ser Tyr Val		
	170		

<210> 333
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 333
 agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50
 atcactgggg gtctccttct gctctgtaca gtggtctatt tctgtagcag 100
 ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150
 agaagtatcc agtgggtggcc atcccctgcc ccatcacata cctaccagtt 200
 tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
 gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300
 aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350
 tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400
 ggtgggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 334
 Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr
 1 5 10 15
 Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
 20 25 30
 Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
 35 40 45
 Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
 50 55 60
 Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
 65 70 75
 Arg Val Gln Phe Leu His Asp Gly Ser Cys
 80 85

<210> 335
 <211> 742
 <212> DNA
 <213> Homo sapiens

<400> 335
 cccgcgcccc gttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50
 ctgctcgcgc cccgcgcgca tggctgcctc cccgcgcgcg cctgctgtcc 100
 tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150
 ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200
 tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250
 tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300
 cccgaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350
 agcgaaatth gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400
 gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450
 gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500
 ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaat 550
 agcgattctc ttcattgtatc tcctaattgcc ttacactact tggtttctga 600

tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
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 cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 336
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 1 5 10 15
 Leu Ala Leu Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
 20 25 30
 Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
 35 40 45
 Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
 50 55 60
 Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
 65 70 75
 Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
 80 85 90
 Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
 95 100 105
 Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
 110 115 120
 Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
 125 130 135
 Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
 140 145

<210> 337
 <211> 1310
 <212> DNA
 <213> Homo sapiens

<400> 337
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 tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg cttgcctgcc 150
 ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200
 gaccactgc ccagccgtc agggacccca acgccatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300
 cccccagcct gagacacaga ggtcaagctg cacagccaga gccagcacg 350
 ggggttcacag caacaccgcc agccccggac tccccgcagg agcccctcgt 400
 gctacggctg aaattcctca atgattcaga gcagggtggc agggcctggc 450
 cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500
 cagcagggtgc gactcatcta ccaagggcag ctgctaggcg acgacacca 550
 gaccctgggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600
 tgtccacgag agtcgggtccc ccaaattccc cctgcccgcc ggggtccgag 650
 cccggccccct ccgggctgga aatcggcagc ctgctgctgc ccctgctgct 700
 cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750
 ttccccctgac cgccactctg ggcttgccg gcttcaccct gctcctcagt 800
 ctctggcct ttgccatgta ccgcccgtag tgctccgcg ggcgcttggc 850
 agcgtgcgcg gccctccgg accttgctcc ccgcgccgcg gcgggagctg 900
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 tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050
 cgactggga gtgggctcct cggggctcgg catctgctgt cgctgcctcg 1100
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 aaaaaaaaa 1310

<210> 338
 <211> 246
 <212> PRT
 <213> Homo sapiens

<400> 338
 Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe
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 Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser
 20 25 30
 Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
 35 40 45

Thr	Pro	Thr	Pro	Ser 50	Gln	Pro	Ser	Ala	Ala 55	Met	Ala	Ala	Thr	Asp 60
Ser	Met	Arg	Gly	Glu 65	Ala	Pro	Gly	Ala	Glu 70	Thr	Pro	Ser	Leu	Arg 75
His	Arg	Gly	Gln	Ala 80	Ala	Gln	Pro	Glu	Pro 85	Ser	Thr	Gly	Phe	Thr 90
Ala	Thr	Pro	Pro	Ala 95	Pro	Asp	Ser	Pro	Gln 100	Glu	Pro	Leu	Val	Leu 105
Arg	Leu	Lys	Phe	Leu 110	Asn	Asp	Ser	Glu	Gln 115	Val	Ala	Arg	Ala	Trp 120
Pro	His	Asp	Thr	Ile 125	Gly	Ser	Leu	Lys	Arg 130	Thr	Gln	Phe	Pro	Gly 135
Arg	Glu	Gln	Gln	Val 140	Arg	Leu	Ile	Tyr	Gln 145	Gly	Gln	Leu	Leu	Gly 150
Asp	Asp	Thr	Gln	Thr 155	Leu	Gly	Ser	Leu	His 160	Leu	Pro	Pro	Asn	Cys 165
Val	Leu	His	Cys	His 170	Val	Ser	Thr	Arg	Val 175	Gly	Pro	Pro	Asn	Pro 180
Pro	Cys	Pro	Pro	Gly 185	Ser	Glu	Pro	Gly	Pro 190	Ser	Gly	Leu	Glu	Ile 195
Gly	Ser	Leu	Leu	Leu 200	Pro	Leu	Leu	Leu	Leu 205	Leu	Leu	Leu	Leu	Leu 210
Trp	Tyr	Cys	Gln	Ile 215	Gln	Tyr	Arg	Pro	Phe 220	Phe	Pro	Leu	Thr	Ala 225
Thr	Leu	Gly	Leu	Ala 230	Gly	Phe	Thr	Leu	Leu 235	Leu	Ser	Leu	Leu	Ala 240
Phe	Ala	Met	Tyr	Arg 245	Pro									

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<210> 339
<211> 849
<212> DNA
<213> Homo sapiens
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atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200
tcaggccagc ctcatcagtc gctgtgactt ggcccaggtg ctgcagctgg 250
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 ccttcccatt tacaactaaa actgaccaga gcccaggaa taaatggttt 750
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<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala
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Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val
				20					25					30

Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser
				35					40					45

Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser
				50					55					60

Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe
				65					70					75

Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser
				80					85					90

Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn
				95					100					105

Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala
				110					115					120

Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly
				125					130					135

Arg	Pro	Leu	Ser	Tyr	Trp	Leu	Thr	Gly	Cys	Arg	Leu	Arg
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140

<210> 341
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 341
ccctccaagg atgacaaagg cgc 23

<210> 342
<211> 29
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-29
<223> Synthetic construct.

<400> 342
ggtcagcagc tttcttgccc taaatcagg 29

<210> 343
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 343
atctcaggcg gcatcctgtc agcc 24

<210> 344
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 344
gtggatgcct gcaagaaggt tggg 24

<210> 345
<211> 45
<212> DNA
<213> Artificial

332

<220>
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 <222> 1-45
 <223> Synthetic construct.

<400> 345
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<210> 346
 <211> 2575
 <212> DNA
 <213> Homo sapiens

<400> 346
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 caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150
 aaggagaaaa ccggggtaaa gggaggggaag caattcaatt tgaagtcctt 200
 gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250
 ggggtgaaac ttgggtcctg tgggttttctg attgtaagtga gaagcaggctc 300
 ttgcacacgc tggttgcaaa tgtcaggacc aggttaagtga actggcagaa 350
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gtgattgact	ggaagacttt	ccagtattac	ccctcaaagg	acctgcagcg	1450
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tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

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20 25 30

Ala Met Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr
35 40 45

Ala Gln Ala Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp
50 55 60

Phe Gly Glu Ser Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly
65 70 75

Glu Glu Tyr Ser Pro Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu
80 85 90

Arg Glu Asp Gln Leu Leu Val Ala Val Ala Leu Pro Gln Ala Arg
95 100 105

Arg Asn Gln Ser Gln Gly Arg Arg Gly Gly Ser Tyr Arg Leu Ile
110 115 120

Lys Gln Pro Arg Arg Gln Asp Lys Glu Ala Pro Lys Arg Asp Trp
125 130 135

Gly Ala Asp Glu Asp Gly Glu Val Ser Glu Glu Glu Glu Leu Thr
140 145 150

Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln Glu Ala Leu Ser Ala
155 160 165

Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val Arg His Pro Leu
170 175 180

Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr Ala Ser Val
185 190 195

Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu Arg Thr
200 205 210

Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys Glu
215 220 225

Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser
230 235 240

Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu
245 250 255

Arg	Ser	Asn	Lys	Arg 260	Leu	Gly	Ala	Ile	Arg 265	Ala	Arg	Met	Leu	Gly 270
Ala	Thr	Arg	Ala	Thr 275	Gly	Asp	Val	Leu	Val 280	Phe	Met	Asp	Ala	His 285
Cys	Glu	Cys	His	Pro 290	Gly	Trp	Leu	Glu	Pro 295	Leu	Leu	Ser	Arg	Ile 300
Ala	Gly	Asp	Arg	Ser 305	Arg	Val	Val	Ser	Pro 310	Val	Ile	Asp	Val	Ile 315
Asp	Trp	Lys	Thr	Phe 320	Gln	Tyr	Tyr	Pro	Ser 325	Lys	Asp	Leu	Gln	Arg 330
Gly	Val	Leu	Asp	Trp 335	Lys	Leu	Asp	Phe	His 340	Trp	Glu	Pro	Leu	Pro 345
Glu	His	Val	Arg	Lys 350	Ala	Leu	Gln	Ser	Pro 355	Ile	Ser	Pro	Ile	Arg 360
Ser	Pro	Val	Val	Pro 365	Gly	Glu	Val	Val	Ala 370	Met	Asp	Arg	His	Tyr 375
Phe	Gln	Asn	Thr	Gly 380	Ala	Tyr	Asp	Ser	Leu 385	Met	Ser	Leu	Arg	Gly 390
Gly	Glu	Asn	Leu	Glu 395	Leu	Ser	Phe	Lys	Ala 400	Trp	Leu	Cys	Gly	Gly 405
Ser	Val	Glu	Ile	Leu 410	Pro	Cys	Ser	Arg	Val 415	Gly	His	Ile	Tyr	Gln 420
Asn	Gln	Asp	Ser	His 425	Ser	Pro	Leu	Asp	Gln 430	Glu	Ala	Thr	Leu	Arg 435
Asn	Arg	Val	Arg	Ile 440	Ala	Glu	Thr	Trp	Leu 445	Gly	Ser	Phe	Lys	Glu 450
Thr	Phe	Tyr	Lys	His 455	Ser	Pro	Glu	Ala	Phe 460	Ser	Leu	Ser	Lys	Ala 465
Glu	Lys	Pro	Asp	Cys 470	Met	Glu	Arg	Leu	Gln 475	Leu	Gln	Arg	Arg	Leu 480
Gly	Cys	Arg	Thr	Phe 485	His	Trp	Phe	Leu	Ala 490	Asn	Val	Tyr	Pro	Glu 495
Leu	Tyr	Pro	Ser	Glu 500	Pro	Arg	Pro	Ser	Phe 505	Ser	Gly	Lys	Leu	His 510
Asn	Thr	Gly	Leu	Gly 515	Leu	Cys	Ala	Asp	Cys 520	Gln	Ala	Glu	Gly	Asp 525
Ile	Leu	Gly	Cys	Pro 530	Met	Val	Leu	Ala	Pro 535	Cys	Ser	Asp	Ser	Arg 540
Gln	Gln	Gln	Tyr	Leu	Gln	His	Thr	Ser	Arg	Lys	Glu	Ile	His	Phe

545	550	555
Gly Ser Pro Gln His Leu Cys Phe Ala	Val Arg Gln Glu Gln Val	
560	565	570
Ile Leu Gln Asn Cys Thr Glu Glu Gly	Leu Ala Ile His Gln Gln	
575	580	585
His Trp Asp Phe Gln Glu Asn Gly Met	Ile Val His Ile Leu Ser	
590	595	600
Gly Lys Cys Met Glu Ala Val Val Gln	Glu Asn Asn Lys Asp Leu	
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Tyr Leu Arg Pro Cys Asp Gly Lys Ala	Arg Gln Gln Trp Arg Phe	
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Asp Gln Ile Asn Ala Val Asp Glu Arg		
635		

<210> 348
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 348
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<210> 349
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 <212> DNA
 <213> Artificial

<220>
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 <222> 1-24
 <223> Synthetic construct.

<400> 349
 ctgtcactgc aaggagccaa cacc 24

<210> 350
 <211> 45
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-45
 <223> Synthetic construct.

<400> 350
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<210> 351
 <211> 2524
 <212> DNA
 <213> Homo sapiens

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cagtcctccc ttcccagcct ccctttgggc ctccctaact ccacctaggc 2200
tgccagggac cggagtcagc tggttcaagg ccatcgggag ctctgcctcc 2250
aagtctaccc ttcccttccc ggactccctc ctgtcccctc ctttccctcc 2300
tccttccttc cactctcctt ccttttgctt cctgcccctt tccccctcct 2350
caggttcttc cctccttctc actgggtttt ccaccttcct ccttcccttc 2400
ttccctggct cctaggctgt gatatatatt tttgtattat ctctttcttc 2450
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tcaaataaag cctttgcaag ataa 2524

<210> 352
<211> 243
<212> PRT
<213> Homo sapiens

<400> 352
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
1 5 10 15

Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
 20 25 30
 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
 35 40 45
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
 50 55 60
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
 65 70 75
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
 80 85 90
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
 95 100 105
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
 110 115 120
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
 125 130 135
 Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
 140 145 150
 Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
 155 160 165
 Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
 170 175 180
 Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
 185 190 195
 Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
 200 205 210
 Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
 215 220 225
 Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
 230 235 240

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

gttaaccagc gcagtcctcc gtgcgtcccg ccgcgcgctg ccctcactcc 50

cggccaggat ggcacctgt ctggccctgc gcatggcgct gctgctggtc 100


```
tccgggggttc tggccctgc ggtgctcaca gacgatgttc cacaggagcc 150
cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200
ccgtgggagag caccagcccc ggccgggagc ccgtggacac cggccccca 250
gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300
ggaccagggc ggcgggtcgc tggggcccg cgctatcgcg gccatcgtga 350
tcgccccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400
ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450
gcggcgcgac tcggcaaaaa aaaaaaaaaa 480
```

```
<210> 354
<211> 121
<212> PRT
<213> Homo sapiens
```

```

<400> 354
Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser
  1          5          10          15

Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu
          20          25          30

Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly
          35          40          45

Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
          50          55          60

Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
          65          70          75

Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro
          80          85          90

Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
          95          100          105

Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
          110          115          120

Ser

```

```
<210> 355
<211> 2134
<212> DNA
<213> Homo sapiens
```

```
<400> 355
ggccgttggt tggcgcgcg ctgaagggtg tggcgcgagc agcgtcggtg 50
ggttgccggc ggcgggccgg gacgggcatg gccctgctgc tgtgcctggt 100
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gtgcctgacg gcggcgctgg cccacggctg tctgcaactg cacagcaact 150
tctccaagaa gttctccttc taccgccacc atgtgaactt caagtcctgg 200
tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250
cgacacgatg aaggagctgc acctggccat ccccgccaag atcacccggg 300
agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350
taccagggga agatgtactt ccccggggtat ttccccaacg agctgcgaaa 400
catcttccgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450
acctggcacc aggagctgg ggaggaggcg agctctccag ggagggaacc 500
agcctagcac ctgaaggatc aatgccatca cccgcggggg acctccccta 550
agtagcccc agaggcgctg ggagtgttg caccgccctc ccctgaagtt 600
tgctccatct cacgctgggg gtcaacctgg ggacccttc cctccgggccc 650
atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700
tggcatcttc cagtacgaga ccattctctg caacaactgc acagactcgc 750
acgtcgctg ctttggttat aactgcgagt agggctcagg catcacacc 800
acccgtgcca gggccctact gtccctgggg tcccaggctc tccttgagg 850
gggtccccc ccttccacct gggtgtcacc gggtagggcg gggccgtgg 900
ttcaggggcg caccattcc aagcctgtgt cccacaggtc ctcggcgag 950
tggaagtcag ctgtccaggg cctcctgaac tacataaata actggcacia 1000
gtaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050
cgtgggtgag tatgtgtggg gcacaggctg gctccctcag ctcccacgtc 1100
ctagaggggc tcccaggag gtggaacctc aaccagctc tgcgcaggag 1150
gcggctgcag tccttttctc cctcaaaggc ctccgacct cagctggagg 1200
cgggcatctt tcctaaaggg tccccatagg gtctggttcc acccatccc 1250
aggtctgtgg tcagagcctg ggagggttcc ctacgatggt taggggtgcc 1300
ccatggaggg gctgactgcc ccacattgcc tttcagacag gacacgagca 1350
tgaggtaagg ccgccctgac ctggacttca gggggagggg gtaaaggag 1400
agaggagggg ggctaggggg tcctctagat cagtgggggc actgcaggtg 1450
gggtctctcc tatacctggg acacctgctg gatgtcacct ctgcaaccac 1500
acccatgtgg tggtttcatg aacagaccac gtcctctgc cttctcctgg 1550

cctgggacac	acagagccac	cccggccttg	tgagtgaccc	agagaaggga	1600
ggcctcggga	gaaggggtgc	tcgtaagcca	acaccagcgt	gccgcggcct	1650
gcacaccctt	cggacatccc	aggcacgagg	gtgtcgtgga	tgtggccaca	1700
cataggacca	cacgtcccag	ctgggaggag	aggcctgggg	ccccaggga	1750
gggaggcagg	gggtggggga	catggagagc	tgaggcagcc	tcgtctcccc	1800
gcagcctggt	atcgccagcc	ttaaggtgtc	tggagcccc	acacttggcc	1850
aacctgacct	tggaagatgc	tgctgagtgt	ctcaagcagc	actgacagca	1900
gctgggcctg	ccccagggca	acgtgggggc	ggagactcag	ctggacagcc	1950
cctgcctgtc	actctggagc	tgggctgctg	ctgcctcagg	accccctctc	2000
cgaccccgga	cagagctgag	ctggccaggg	ccaggagggc	gggagggagg	2050
gaatgggggt	gggctgtgcg	cagcatcagc	gcctgggcag	gtccgcagag	2100
ctgcgggatg	tgattaaagt	ccctgatgtt	tctc	2134	

<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

Met Ala Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala
1 5 10 15

His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser
20 25 30

Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp
35 40 45

Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr
50 55 60

Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu
65 70 75

Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln
80 85 90

Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu
95 100 105

Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala
110 115 120

Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln
125 130 135

Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

140

145

150

Ser Pro Arg Gly Asp Leu Pro
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

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cctcttattt ctctcacgt gtgagctggc tgcagaagtt gctgcagaag 100
ttgagaaatc ctcatggtt cctgggtgtg cccaggaacc cacgtggctc 150
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200
cataggcttc ttccaggatt tagaaatacc agcagtgcc atactccata 250
gcatggtgca aaaattccca ggcggtgcat ttgggatcag cactgattct 300
gaggttctga cactactaca catcactggg aacaccatct gcctctttcg 350
cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400
ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500
tcagattcat ctctctctga taatgaacaa ggctctccca gagtatgaag 550
agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
ctctttattc tgggtggacag tggtatgaaa gaaaatggga aggtgatatc 650
atcttttcaa cttaaaggagt ctcaactgcc agctttggca atttaccaga 700
ctctagatga cgagtgggat aactgcccc cagcagaagt ttccgtagag 750
catgtgcaaa acttttgtga tggattccta agtggaaaat tgttgaaaga 800
aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850
ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900
aactcaaate tcagagacac taaacaacag gatcactagg cctgccaacc 950
acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000
gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050
tctcttcttc cttcttttaa atttcatatc ctactccct atccaatttc 1100
cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150
tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200

```
ctagagaaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250
cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300
gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350
tcaaaaacca aaggatggtt ttaaacacct ttgtgaaatt gtctttttgc 1400
cagaagttaa aggctgtctc caagtccttg aactcagcag aaatagacca 1450
tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaataca 1500
caacctgcat aataaataaa aggcaatcat gttata 1536
```

```
<210> 358
<211> 273
<212> PRT
<213> Homo sapiens
```

<400>	358													
Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu
1				5					10					15
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser
				20					25					30
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp
				35					40					45
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val
				50					55					60
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu
				65					70					75
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser
				80					85					90
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr
				95					100					105
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu
				110					115					120
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe
				125					130					135
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val
				140					145					150
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu
				155					160					165
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His
				170					175					180
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe
				185					190					195

Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val Ile Ser
200 205 210

Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile Tyr
215 220 225

Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val
230 235 240

Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe Leu Ser Gly
245 250 255

Lys Leu Leu Lys Glu Asn Arg Glu Ser Glu Gly Lys Thr Pro Lys
260 265 270

Val Glu Leu

<210> 359

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 359

ccagcagtgc ccatactcca tagc 24

<210> 360

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 360

tgacgagtgg gatacactgc 20

<210> 361

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 361

gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 362
 attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
 <211> 1777
 <212> DNA
 <213> Homo sapiens

<400> 363
 ggagagccgc ggctgggacc ggagtgggga ggcgggctg gaggtgccac 50
 ccggcgcggg tggcggagag atcagaagcc tcttcccaa gccgagcaa 100
 cctcagcggg gaccggggt cagggacgcg gcggcgggcg cggcgactgc 150
 agtggttga cgatggcagc gtccgccgga gccggggcg tgattgcagc 200
 cccagacagc cggcgctggc tgtggtcggg gctggcgggc gcgcttgggc 250
 tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300
 ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350
 tagtacgact ggcggttga cctcagtctc ctggagcttc cagccagagg 400
 gggccgacac tactgtgtcg tttttocact actcccaagg gcaagtgtac 450
 cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
 tgacaagaaa gatgcatcaa tcaacataga aaatatgcag ttatacaca 550
 atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600
 cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgctgtgtt 650
 tccagtttgg gtagtggtgg gcatagttac tgctgtggtc ctaggctctca 700
 ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750
 aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800
 gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850
 tgccttctgg atctcaccag ggcccagtca tatatgcaca gttagaccac 900
 tccggcgagc atcacagtga caagattaac aagtcagagt ctgtggtgta 950
 tgcggatatc cgaaagaatt aagagaatac ctagaacata tctcagcaa 1000

gaaacaaaac	caaactggac	tctcgtgcag	aaaatgtagc	ccattaccac	1050
atgtagcctt	ggagacccag	gcaaggacaa	gtacacgtgt	actcacagag	1100
ggagagaaaag	atgtgtacaa	aggatatgta	taaatattct	atttagtcat	1150
cctgatatga	ggagccagt	ttgcatgatg	aaaagatggt	atgattctac	1200
atatgtaccc	attgtcttgc	tgtttttgta	ctttcttttc	aggtcattta	1250
caattgggag	atttcagaaa	cattcctttc	accatcattt	agaaatgggt	1300
tgcccttaatg	gagacaatag	cagatcctgt	agtattttcca	gtagacatgg	1350
cctttttaatc	taagggctta	agactgatta	gtccttagcat	ttactgtagt	1400
tggaggatgg	agatgctatg	atggaagcat	accagggtg	gccttttagca	1450
cagtatcagt	accattttatt	tgtctgccgc	ttttaaaaaa	taccatttgg	1500
ctatgccact	tgaaaacaat	ttgagaagtt	tttttgaagt	ttttctcact	1550
aaaatatggg	gcaattgtta	gccttacatg	ttgtgtagac	ttactttaag	1600
tttgcaccct	tgaaatgtgt	catatcaatt	tctggattca	taatagcaag	1650
attagcaaag	gataaatgcc	gaaggtcact	tcattctgga	cacagttgga	1700
tcaatactga	ttaagtagaa	aatccaagct	ttgcttgaga	acttttgtaa	1750
cgtggagagt	aaaaagtatc	ggtttta	1777		

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<210> 364
<211> 269
<212> PRT
<213> Homo sapiens
```

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<400> 364
Met  Ala  Ala  Ser  Ala  Gly  Ala  Gly  Ala  Val  Ile  Ala  Ala  Pro  Asp
 1          5          10          15

Ser  Arg  Arg  Trp  Leu  Trp  Ser  Val  Leu  Ala  Ala  Ala  Leu  Gly  Leu
          20          25          30

Leu  Thr  Ala  Gly  Val  Ser  Ala  Leu  Glu  Val  Tyr  Thr  Pro  Lys  Glu
          35          40          45

Ile  Phe  Val  Ala  Asn  Gly  Thr  Gln  Gly  Lys  Leu  Thr  Cys  Lys  Phe
          50          55          60

Lys  Ser  Thr  Ser  Thr  Thr  Gly  Gly  Leu  Thr  Ser  Val  Ser  Trp  Ser
          65          70          75

Phe  Gln  Pro  Glu  Gly  Ala  Asp  Thr  Thr  Val  Ser  Phe  Phe  His  Tyr
          80          85          90

Ser  Gln  Gly  Gln  Val  Tyr  Leu  Gly  Asn  Tyr  Pro  Pro  Phe  Lys  Asp
          95          100          105

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Arg Ile Ser Trp Ala Gly Asp Leu Asp Lys Lys Asp Ala Ser Ile
110 115 120

Asn Ile Glu Asn Met Gln Phe Ile His Asn Gly Thr Tyr Ile Cys
125 130 135

Asp Val Lys Asn Pro Pro Asp Ile Val Val Gln Pro Gly His Ile
140 145 150

Arg Leu Tyr Val Val Glu Lys Glu Asn Leu Pro Val Phe Pro Val
155 160 165

Trp Val Val Val Gly Ile Val Thr Ala Val Val Leu Gly Leu Thr
170 175 180

Leu Leu Ile Ser Met Ile Leu Ala Val Leu Tyr Arg Arg Lys Asn
185 190 195

Ser Lys Arg Asp Tyr Thr Gly Cys Ser Thr Ser Glu Ser Leu Ser
200 205 210

Pro Val Lys Gln Ala Pro Arg Lys Ser Pro Ser Asp Thr Glu Gly
215 220 225

Leu Val Lys Ser Leu Pro Ser Gly Ser His Gln Gly Pro Val Ile
230 235 240

Tyr Ala Gln Leu Asp His Ser Gly Gly His His Ser Asp Lys Ile
245 250 255

Asn Lys Ser Glu Ser Val Val Tyr Ala Asp Ile Arg Lys Asn
260 265

<210> 365
<211> 1321
<212> DNA
<213> Homo sapiens

<400> 365
gccggctgtg cagagacgcc atgtaccggc tcctgtcagc agtgactgcc 50
cgggctgccg cccccggggg cttggcctca agctgcggac gacgcggggg 100
ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggc 150
tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
aggggcgcgg ccccgccgca gtccccgcg gcccccgacc ctgagggcgtc 250
gcctctggcc gagccgccac aggagcagtc cctcgccccg tgggtctccgc 300
agaccccggc gccgccctgc tccaggtgct tcgccagagc catcgagagc 350
agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400
agtggttgga gtttctgtag atggaaaaga agtctggtca gaaggtttag 450
gttatgctga tgttgagaac cgtgtacat gtaaaccaga gacagttatg 500

cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550
gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600
ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650
agattactga tttcccattt aagtggaatt cgtcattatg aaaaggacat 700
aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
gattttacta aatttaaaac agagcaggag aatgaagcca aatgccggaa 850
ttcaaaacct ggcaagaaaa agaatgattt tgaacaaggc gaattatatt 900
tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaaat 950
gatcctttgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000
ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050
tggaactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100
caggaagaaa acgagccagt gattttacaat agagcaagggt aaatgaatac 1150
cttctgctgt gtctagctat atcgcatctt aacactattht tattaattaa 1200
aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacatttttg 1250
gagcttttct acatgtctgt tttctcatct gttaaagtga ggaagtaaaa 1300
catgtttata aagtaaaaaa a 1321

```
<210> 366
<211> 373
<212> PRT
<213> Homo sapiens
```

```

<400> 366
Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro
  1      5      10      15
Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg
      20      25      30
Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly
      35      40      45
Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu
      50      55      60
Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu
      65      70      75
Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro
      80      85      90

```

Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala
95 100 105

Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp
110 115 120

Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly
125 130 135

Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn
140 145 150

Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile
155 160 165

Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala
170 175 180

Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu
185 190 195

Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr
200 205 210

Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys
215 220 225

Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys
230 235 240

Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys
245 250 255

Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu
260 265 270

Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn
275 280 285

Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn
290 295 300

Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe
305 310 315

Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu
320 325 330

Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp
335 340 345

Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val
350 355 360

Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg
365 370

<210> 367

<211> 30
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-30
<223> Synthetic construct.

<400> 367
tggaagagaa gtctgggtcag aaggtttagg 30

<210> 368
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 368
catttggtt cattctcctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 369
aaaacctcag aacaactcat ttgcacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 370
gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100
ctggggcaac ccggctgctc ctgctcttgc tgatggcggt agcagcgccc 150
agtcgagccc ggggcagcgg ctgccggggc gggactgggt cgcgaggggc 200
tggggcgga ggtcgagagg gcgaggcctg tggcacgggt gggctgctgc 250
tggagcactc atttgagatc gatgacagt ccaacttccg gaagcggggc 300
tcaactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350
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<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met Ala Ala Ala Ser Ala Gly Ala Thr Arg Leu Leu Leu Leu Leu
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Leu Met Ala Val Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys
20 25 30

Arg Ala Gly Thr Gly Ala Arg Gly Ala Gly Ala Glu Gly Arg Glu
35 40 45

Gly Glu Ala Cys Gly Thr Val Gly Leu Leu Leu Glu His Ser Phe
50 55 60

Glu Ile Asp Asp Ser Ala Asn Phe Arg Lys Arg Gly Ser Leu Leu
65 70 75

Trp Asn Gln Gln Asp Gly Thr Leu Ser Leu Ser Gln Arg Gln Leu
80 85 90

Ser Glu Glu Glu Arg Gly Arg Leu Arg Asp Val Ala Ala Leu Asn
95 100 105

Gly Leu Tyr Arg Val Arg Ile Pro Arg Arg Pro Gly Ala Leu Asp
110 115 120

Gly Leu Glu Ala Gly Gly Tyr Val Ser Ser Phe Val Pro Ala Cys
125 130 135

Ser Leu Val Glu Ser His Leu Ser Asp Gln Leu Thr Leu His Val
140 145 150

Asp Val Ala Gly Asn Val Val Gly Val Ser Val Val Thr His Pro
155 160 165

Gly Gly Cys Arg Gly His Glu Val Glu Asp Val Asp Leu Glu Leu
170 175 180

Phe Asn Thr Ser Val Gln Leu Gln Pro Pro Thr Thr Ala Pro Gly
185 190 195

Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu Gln Ala
200 205 210

Gln Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala Lys
215 220 225

Tyr Trp Met Tyr Ile Ile Pro Val Val Leu Phe Leu Met Met Ser
230 235 240

Gly Ala Pro Asp Thr Gly Gly Gln Gly Gly Gly Gly Gly Gly
245 250 255

Gly Gly Gly Gly Ser Gly Leu Cys Cys Val Pro Pro Ser Leu
260 265

<210> 373
<211> 1706
<212> DNA
<213> Homo sapiens

<400> 373
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cagcaggtcg tccggggggc caccatgctg gtgactgcct accttgcttt 150
tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200

ctaaaccccc tggaagggcc tgcagcaatc cctccttcct tcggtttcaa 250
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cctctttctc ctgacttact cactatgctg cttaaccaaa ctctctcaag 500
actactttgt gctgctagtg gggcgagcac ttgggtgggt gtccacagcc 550
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gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600
gggaggacat gatgggggtg atggactgga aagaaggctc caaaagttcc 1650

ctctgtgtta ctccattta gaaaataaac actttttaaat gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser	
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Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly	
				20					25					30	
Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe	
				35					40					45	
Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala	
				50					55					60	
Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly	
				65					70					75	
Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu	
				80					85					90	
Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys	
				95					100					105	
Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu	
				110					115					120	
Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala	
				125					130					135	
Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala	
				140					145					150	
Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu	
				155					160					165	
Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val	
				170					175					180	
Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp	
				185					190					195	
Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu	
				200					205					210	
Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn	
				215					220					225	
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu	
				230					235					240	

Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile
245 250 255

Gln Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp
260 265 270

Thr Pro Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe
275 280 285

Ser Ser Phe Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg
290 295 300

Ile Ala Thr Ser Lys Arg Tyr His Leu Gln Pro Met His Leu Leu
305 310 315

Ser Leu Ala Val Leu Ile Val Val Phe Ser Leu Phe Met Leu Thr
320 325 330

Phe Ser Thr Ser Pro Gly Gln Glu Ser Pro Val Glu Ser Phe Ile
335 340 345

Ala Phe Leu Leu Ile Glu Leu Ala Cys Gly Leu Tyr Phe Pro Ser
350 355 360

Met Ser Phe Leu Arg Arg Lys Val Ile Pro Glu Thr Glu Gln Ala
365 370 375

Gly Val Leu Asn Trp Phe Arg Val Pro Leu His Ser Leu Ala Cys
380 385 390

Leu Gly Leu Leu Val Leu His Asp Ser Asp Arg Lys Thr Gly Thr
395 400 405

Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met Val Met Ala Leu
410 415 420

Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His Asp Ala Glu
425 430 435

Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro Glu Leu
440 445 450

<210> 375
<211> 1098
<212> DNA
<213> Artificial

<400> 375
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gctccccgcg tgcgtcgcg cccacggctt ccgtatccat gattatttgt 150
actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200
cctgccaagg actttggtgg tatctttcac acaaggtatg agcagattca 250

ccttgtcccc	gctgaacctc	cagaggcctg	cggggaactc	agcaacggtt	300
tcttcatcca	ggaccagatt	gctctggtgg	agaggggggg	ctgctccttc	350
ctctccaaga	ctcgggtggt	ccaggagcac	ggcgggcggg	cggtgatcat	400
ctctgacaac	gcagttgaca	atgacagctt	ctacgtggag	atgatccagg	450
acagtaccca	gcgcacagct	gacatccccg	ccctcttcct	gctcggccga	500
gacggctaca	tgatccgccg	ctctctggaa	cagcatgggc	tgccatgggc	550
catcatttcc	atcccagtc	atgtcaccag	catccccacc	tttgagctgc	600
tgcaaccgcc	ctggaccttc	tggtagaaga	gtttgtccca	cattccagcc	650
ataagtgact	ctgagctggg	aaggggaaac	ccaggaattt	tgctacttgg	700
aatttgagga	tagcatctgg	ggacaagtgg	agccaggtag	aggaaaaggg	750
tttgggcgtt	gctaggctga	aagggaagcc	acaccactgg	ccttcccttc	800
cccagggccc	ccaaggggtg	ctcatgtctac	aagaagaggc	aagagacagg	850
ccccagggct	tctggctaga	accgaaaca	aaaggagctg	aaggcaggtg	900
gcctgagagc	catctgtgac	ctgtcacact	cacctggctc	cagcctcccc	950
taccaggggt	ctctgcacag	tgaccttcac	agcagttgtt	ggagtggttt	1000
aaagagctgg	tgtttgggga	ctcaataaac	cctcactgac	tttttagcaa	1050
taaagcttct	catcaggggt	gcaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaa	1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu
1 5 10 15

Pro Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu
20 25 30

Tyr Phe Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr
35 40 45

Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr
50 55 60

Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly
65 70 75

Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val
80 85 90

Glu	Arg	Gly	Gly	Cys 95	Ser	Phe	Leu	Ser	Lys 100	Thr	Arg	Val	Val	Gln 105
Glu	His	Gly	Gly	Arg 110	Ala	Val	Ile	Ile	Ser 115	Asp	Asn	Ala	Val	Asp 120
Asn	Asp	Ser	Phe	Tyr 125	Val	Glu	Met	Ile	Gln 130	Asp	Ser	Thr	Gln	Arg 135
Thr	Ala	Asp	Ile	Pro 140	Ala	Leu	Phe	Leu	Leu 145	Gly	Arg	Asp	Gly	Tyr 150
Met	Ile	Arg	Arg	Ser 155	Leu	Glu	Gln	His	Gly 160	Leu	Pro	Trp	Ala	Ile 165
Ile	Ser	Ile	Pro	Val 170	Asn	Val	Thr	Ser	Ile 175	Pro	Thr	Phe	Glu	Leu 180
Leu	Gln	Pro	Pro	Trp 185	Thr	Phe	Trp							

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<210> 377
<211> 496
<212> DNA
<213> Artificial
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<220>  
<221> unsure  
<222> 396  
<223> unknown base
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<400> 377
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ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100
ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctctccta 150
ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200
atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250
aagaccacgg ggtgcggcat ctacaaggac aacaacaaaa gcagcatata 300
ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496
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<210> 378
<211> 116
<212> PRT
<213> Homo sapiens
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<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20					25						30
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35					40						45
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50					55						60
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65					70						75
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80					85						90
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95					100						105
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu				
			110					115						

<210> 379

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 380

cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln
50 55 60

Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly
65 70 75

Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr
80 85 90

Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met
95 100 105

Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly
110 115 120

Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val
125 130 135

Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly
140 145 150

Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro
155 160 165

Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg
170 175

<210> 384
<211> 2379
<212> DNA
<213> Homo sapiens

<400> 384
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atacagatgt ggcagctcag gtagcccca attgcctgga agaatacatc 150
atgttttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
cccccccca ccccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250
atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300
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caatattgac	gaaaatgctt	ttaatggaat	acgcagactc	aaagagctga	850
ttcttagttc	caatagaatc	tcctat	ttacaatac	cttcagacct	900
gtgacaaatt	tacggaactt	ggatctgtcc	tataatcagc	tgcattctct	950
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cgccctcaacc	tggattccaa	caagctcaca	tttattgg	aagagatttt	1400
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aatgcagcag	aaatatttgc	tcccttgtaa	actggctgaa	aagttttaa	1500
ggtctaagg	agaatacaat	tatctgtgcc	agtcccaaag	agctgcaagg	1550
agtaa	atcgatgcag	tgaagaacta	cagcatctgt	ggcaaaagta	1600
ctacagagag	gtttgatctg	gccagggctc	tcccaaagcc	gacgtttaag	1650
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ctcgtcatcc	tgctggttat	ctacgtgtca	tggaâgcgg	accctg	1850
catgaagcag	ctgcagcagc	gctccctcat	gcgaaggcac	aggaaaaaga	1900
aaagacagtc	cctaaagcaa	atgactccca	gcaccagga	attttatgta	1950
gattataaac	ccaccaacac	ggagaccagc	gagatgctgc	tgaatgggac	2000
gggaccctgc	acctataaca	aatcgggctc	cagggagtgt	gaggtatgaa	2050
ccattgtgat	aaaaagagct	cttaaaagct	gggaaataag	tggtgcttta	2100

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 aaataaccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300
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 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385
 <211> 513
 <212> PRT
 <213> Homo sapiens

<400> 385
 Met Gly Phe Asn Val Ile Arg Leu Leu Ser Gly Ser Ala Val Ala
 1 5 10 15
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 20 25 30
 Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
 35 40 45
 Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
 50 55 60
 Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
 65 70 75
 Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
 80 85 90
 Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
 95 100 105
 Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
 110 115 120
 Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
 125 130 135
 Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
 140 145 150
 Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg
 155 160 165
 Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys
 170 175 180
 Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser
 185 190 195
 Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu

200										205					210				
His	Leu	Glu	His	Asn	Gln	Phe	Ser	Lys	Leu	Asn	Leu	Ala	Leu	Phe					
				215					220					225					
Pro	Arg	Leu	Val	Ser	Leu	Gln	Asn	Leu	Tyr	Leu	Gln	Trp	Asn	Lys					
				230					235					240					
Ile	Ser	Val	Ile	Gly	Gln	Thr	Met	Ser	Trp	Thr	Trp	Ser	Ser	Leu					
				245					250					255					
Gln	Arg	Leu	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Ala	Phe	Ser	Gly					
				260					265					270					
Pro	Ser	Val	Phe	Gln	Cys	Val	Pro	Asn	Leu	Gln	Arg	Leu	Asn	Leu					
				275					280					285					
Asp	Ser	Asn	Lys	Leu	Thr	Phe	Ile	Gly	Gln	Glu	Ile	Leu	Asp	Ser					
				290					295					300					
Trp	Ile	Ser	Leu	Asn	Asp	Ile	Ser	Leu	Ala	Gly	Asn	Ile	Trp	Glu					
				305					310					315					
Cys	Ser	Arg	Asn	Ile	Cys	Ser	Leu	Val	Asn	Trp	Leu	Lys	Ser	Phe					
				320					325					330					
Lys	Gly	Leu	Arg	Glu	Asn	Thr	Ile	Ile	Cys	Ala	Ser	Pro	Lys	Glu					
				335					340					345					
Leu	Gln	Gly	Val	Asn	Val	Ile	Asp	Ala	Val	Lys	Asn	Tyr	Ser	Ile					
				350					355					360					
Cys	Gly	Lys	Ser	Thr	Thr	Glu	Arg	Phe	Asp	Leu	Ala	Arg	Ala	Leu					
				365					370					375					
Pro	Lys	Pro	Thr	Phe	Lys	Pro	Lys	Leu	Pro	Arg	Pro	Lys	His	Glu					
				380					385					390					
Ser	Lys	Pro	Pro	Leu	Pro	Pro	Thr	Val	Gly	Ala	Thr	Glu	Pro	Gly					
				395					400					405					
Pro	Glu	Thr	Asp	Ala	Asp	Ala	Glu	His	Ile	Ser	Phe	His	Lys	Ile					
				410					415					420					
Ile	Ala	Gly	Ser	Val	Ala	Leu	Phe	Leu	Ser	Val	Leu	Val	Ile	Leu					
				425					430					435					
Leu	Val	Ile	Tyr	Val	Ser	Trp	Lys	Arg	Tyr	Pro	Ala	Ser	Met	Lys					
				440					445					450					
Gln	Leu	Gln	Gln	Arg	Ser	Leu	Met	Arg	Arg	His	Arg	Lys	Lys	Lys					
				455					460					465					
Arg	Gln	Ser	Leu	Lys	Gln	Met	Thr	Pro	Ser	Thr	Gln	Glu	Phe	Tyr					
				470					475					480					
Val	Asp	Tyr	Lys	Pro	Thr	Asn	Thr	Glu	Thr	Ser	Glu	Met	Leu	Leu					
				485					490					495					

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
 500 505 510

Cys Glu Val

<210> 386
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 386
 ctgggatctg aacagtttcg gggc 24

<210> 387
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 387
 ggtccccagg acatggtctg tccc 24

<210> 388
 <211> 48
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.

<400> 388
 gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
 <211> 1449
 <212> DNA
 <213> Homo sapiens

<400> 389
 agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
 ttgactgtcc tttaaataatg tcaagatcca gacttttcag tgtcacctca 100
 gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150
 ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacacccctaa tggctggtat atctggatcc tcctgctgct ggttttgggtg 250
gcagctcttc tctgtggagc tgtggctcctc tgcctccagt gctggctgag 300
gagaccccgga attgattctc acaggcgcac catggcagtt tttgctgttg 350
gagacttggga ctctatattat gggacagaag cagctgtgag tccaactgtt 400
ggaattcacc ttcaaactca aaccctgac ctatatacctg ttctgctcc 450
atgttttggc cctttaggct cccacctcc atatgaagaa attgtaaaaa 500
caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600
tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650
ggatgttggga aaaaattttg gtcattggaga tgtttaaata gttaaagtagc 700
aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750
attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800
gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850
tctgctttaa actctttcct agcatggggt ccataaaaat tattataatt 900
taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950
agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000
tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050
gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100
ttagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150
ccaacacggg gagaaaaagaa aatttccct tttacagtaa tgaatgtggc 1200
ctccatagtc catagtgttt ctctggagcc tcagggcttg gcatttattg 1250
cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300
gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350
agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400
ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390
<211> 146
<212> PRT
<213> Homo sapiens

<400> 390
Met Ser Arg Ser Arg Leu Phe Ser Val Thr Ser Ala Ile Ser Thr
1 5 10 15

Ile Gly Ile Leu Cys Leu Pro Leu Phe Gln Leu Val Leu Ser Asp
20 25 30
Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln
35 40 45
His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Val Leu
50 55 60
Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys
65 70 75
Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala
80 85 90
Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala
95 100 105
Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro
110 115 120
Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser
125 130 135
Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr
140 145

<210> 391
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 391
cttttcagtg tcacctcagc gatctc 26

<210> 392
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 392
ccaaaacatg gagcaggaac agg 23

<210> 393
<211> 47
<212> DNA
<213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-47
 <223> Synthetic construct.

<400> 393
 ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
 <211> 2340
 <212> DNA
 <213> Homo sapiens

<400> 394
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 aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200
 tctctttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250
 ctcttcaaaa ctcatctcct ggggtgactga gttaatagag tggatacaac 300
 cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350
 ttttcaagtc ttgatttgtg gcttacctca agttaccatt tttcagtcaa 400
 gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
 tatgtcccag aaattgagtt tactgttgct tgtatttgga ctcatgtggg 500
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 gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600
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 cagtaaccac aaataaaaga acgaatgtct cgggcagtat cagatagcag 850
 ttgaaaatca ccttgtgctg ctccatccac tgtggattat atcctatggc 900
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 aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100

aagcagatag gtgagttttg tataaatctt ttgtgtttga gatcaagctg 1150
aatgaaaac actgaaaaac atggattcat ttctataaca catttattta 1200
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tgcttattgt actatatttt gttattccaa ttatgagcag agaaaggaaa 1350
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tatgaagatt gactatcttt tcaggaaaaa agctgtatat agcacaggga 2000
accctaactc tgggtaattc tagtataaaa caaattatac ttttatttaa 2050
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tatttattct ctatagtaac tgcttaagtg cagctagctt ctagatttag 2150
actatataga atttagatat tgtattgttc gtcattataa tatgctacca 2200
catgtagcaa taattacaat attttattaa aataaatatg tgaaatattg 2250
tttcatgaaa gacagatttc caaatctctc ttctcttctc tgtactgtct 2300
acctttatgt gaagaaatta attatatgcc attgccaggt 2340

<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser
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atgggaaccc	tctagctgtc	attgggtccg	gtgccttcgc	ggggctggga	750
ggccttacac	acctgtctct	ggccagcctg	cagaggctcc	ctgagctggc	800
gcccagtggc	ttccgtgagc	taccgggcct	gcaggtcctg	gacctgtcgg	850
gcaaccccaa	gcttaactgg	gcaggagctg	aggtgttttc	aggcctgagc	900
tccctgcagg	agctggacct	ttcgggcacc	aacctggtgc	ccctgcctga	950
ggcgctgctc	ctccacctcc	cggcactgca	gagcgtcagc	gtgggccagg	1000
atgtgcggtg	ccggcgccctg	gtgcggggagg	gcacctaccc	ccggaggcct	1050
ggctccagcc	ccaaggtgcc	cctgcactgc	gtagacaccc	gggaatctgc	1100
tgccaggggc	cccaccatct	tgtgacaaat	ggtgtggccc	agggccacat	1150
aacagactgc	tgtcctgggc	tgctcaggt	cccagtaac	ttatgttcaa	1200
tgtgccaaca	ccagtgggga	gcccgcaggc	ctatgtggca	gcgtcaccac	1250
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gcctcctgcc	tcccagccc	gacccaatgc	actttcttgt	ctcctctaata	1800
aagccccacc	ctccccgcct	gggtccccc	tgctgccctt	gcctgttccc	1850
cattagcaca	ggagtagcag	cagcaggaca	ggcaagagcc	tcacaagtgg	1900
gactctgggc	ctctgaccag	ctgtgcggca	tgggctaagt	cactctgccc	1950
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ctcacccctg	gttggggctc	cccagcatcc	agactggaaa	cctacccatt	2050
ttcccctgag	catcctctag	atgctgcccc	aaggagttgc	tgcagttctg	2100

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 aagctgggca tcagtggcca catgggcatc aggggctggc cccacagaga 2500
 cccacaggg cagtgaagctc tgtcttcccc cacctgccta gcccacatc 2550
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 aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 2639

<210> 397
 <211> 353
 <212> PRT
 <213> Homo sapiens

<400> 397
 Met Pro Trp Pro Leu Leu Leu Leu Ala Val Ser Gly Ala Gln
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 Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser
 35 40 45
 Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
 50 55 60
 Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu
 65 70 75
 Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp
 80 85 90
 Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser
 95 100 105
 Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu
 110 115 120
 Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp
 125 130 135
 Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala
 140 145 150

Phe	Thr	Thr	His	Ser 155	Gln	Gly	Arg	Ala	Leu 160	His	Val	Asp	Leu	Ser 165
His	Asn	Leu	Ile	His 170	Arg	Leu	Val	Pro	His 175	Pro	Thr	Arg	Ala	Gly 180
Leu	Pro	Ala	Pro	Thr 185	Ile	Gln	Ser	Leu	Asn 190	Leu	Ala	Trp	Asn	Arg 195
Leu	His	Ala	Val	Pro 200	Asn	Leu	Arg	Asp	Leu 205	Pro	Leu	Arg	Tyr	Leu 210
Ser	Leu	Asp	Gly	Asn 215	Pro	Leu	Ala	Val	Ile 220	Gly	Pro	Gly	Ala	Phe 225
Ala	Gly	Leu	Gly	Gly 230	Leu	Thr	His	Leu	Ser 235	Leu	Ala	Ser	Leu	Gln 240
Arg	Leu	Pro	Glu	Leu 245	Ala	Pro	Ser	Gly	Phe 250	Arg	Glu	Leu	Pro	Gly 255
Leu	Gln	Val	Leu	Asp 260	Leu	Ser	Gly	Asn	Pro 265	Lys	Leu	Asn	Trp	Ala 270
Gly	Ala	Glu	Val	Phe 275	Ser	Gly	Leu	Ser	Ser 280	Leu	Gln	Glu	Leu	Asp 285
Leu	Ser	Gly	Thr	Asn 290	Leu	Val	Pro	Leu	Pro 295	Glu	Ala	Leu	Leu	Leu 300
His	Leu	Pro	Ala	Leu 305	Gln	Ser	Val	Ser	Val 310	Gly	Gln	Asp	Val	Arg 315
Cys	Arg	Arg	Leu	Val 320	Arg	Glu	Gly	Thr	Tyr 325	Pro	Arg	Arg	Pro	Gly 330
Ser	Ser	Pro	Lys	Val 335	Pro	Leu	His	Cys	Val 340	Asp	Thr	Arg	Glu	Ser 345
Ala	Ala	Arg	Gly	Pro 350	Thr	Ile	Leu							

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<210> 398
<211> 23
<212> DNA
<213> Artificial
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<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.
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<400> 398
ccctgccagc cgagagcttc acc 23
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<210>	399
<211>	23
<212>	DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caacccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

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gtgggtctga ggggaccaga aggtgagct acgttggctt tctggaagg 100

gaggctatat gcgtcaattc cccaaaacaa gttttgacat tccccctgaa 150

atgtcattct ctatctattc actgcaagt cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc cacaaacctt caggaaatac gaaatggatt 500

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 atttttgtaa tatctttctg ctattggata tttttattag ttaatatatt 1150
 tttttatttt ttgctattta atgtatttat ttttttactt ggacatgaaa 1200
 ctttaaaaaa attcacagat tataattata acctgactag agcaggtgat 1250
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 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
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 ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
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 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

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Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
			20					25					30	
Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
			35					40					45	
Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu
			50					55					60	
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu
			65					70					75	
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser
			80					85					90	

Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Thr
 95 100 105
 Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile
 110 115 120
 Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Glu Ile Arg
 125 130 135
 Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile Leu
 140 145 150
 Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys
 155 160 165
 Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe
 170 175 180
 Lys Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser
 185 190 195
 Ser Leu Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu
 200 205 210
 Ser His Ala His Met Thr Cys His Cys Gly Glu Glu Ala Met Lys
 215 220 225
 Lys Tyr Ser Gln Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln
 230 235 240
 Ala Ala Val Val Lys Ala Leu Gly Glu Leu Asp Ile Leu Leu Gln
 245 250 255
 Trp Met Glu Glu Thr Glu
 260

<210> 403
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-28
 <223> Synthetic construct.

<400> 403
 ctccctgtggt ctccagattt caggccta 28

<210> 404
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 404
agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50
aggcttttgc cgctgacca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggctaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
cacccgcat ttacagacac gtagtgtatt ctggaggctcg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tcccctttgg aaatcagtca ttggagggat gatggctggt gttattggcc 450
agtttttagc caatccaact gacctagtga aggttcagat gcaaattgaa 500
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600
gctgggtacc caatatacaa agagcagcac tggatgaatat gggagattta 650
accacttatg atacagtga acactacttg gtattgaata caccacttga 700
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
gctttttacc atcttggtg agaatgacct cttggtcaat ggtgttctgg 950
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

Arg Trp Pro Arg Ala Ser Lys Phe Leu Leu Ser Gly Cys Ala Ala
 20 25 30
 Thr Val Ala Glu Leu Ala Thr Phe Pro Leu Asp Leu Thr Lys Thr
 35 40 45
 Arg Leu Gln Met Gln Gly Glu Ala Ala Leu Ala Arg Leu Gly Asp
 50 55 60
 Gly Ala Arg Glu Ser Ala Pro Tyr Arg Gly Met Val Arg Thr Ala
 65 70 75
 Leu Gly Ile Ile Glu Glu Glu Gly Phe Leu Lys Leu Trp Gln Gly
 80 85 90
 Val Thr Pro Ala Ile Tyr Arg His Val Val Tyr Ser Gly Gly Arg
 95 100 105
 Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly Lys Ser
 110 115 120
 Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly Met
 125 130 135
 Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu
 140 145 150
 Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly
 155 160 165
 Lys Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile
 170 175 180
 Leu Ala Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val Pro
 185 190 195
 Asn Ile Gln Arg Ala Ala Leu Val Asn Met Gly Asp Leu Thr Thr
 200 205 210
 Tyr Asp Thr Val Lys His Tyr Leu Val Leu Asn Thr Pro Leu Glu
 215 220 225
 Asp Asn Ile Met Thr His Gly Leu Ser Ser Leu Cys Ser Gly Leu
 230 235 240
 Val Ala Ser Ile Leu Gly Thr Pro Ala Asp Val Ile Lys Ser Arg
 245 250 255
 Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr
 260 265 270
 Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly
 275 280 285
 Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met
 290 295 300
 Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg

305

310

315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407
<211> 31
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-31
<223> Synthetic construct.

<400> 407
cgcgatccc gttatcgtct tgcgctactg c 31

<210> 408
<211> 34
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-34
<223> Synthetic construct.

<400> 408
gcggaattct taaaatggac tgactccact catc 34

<210> 409
<211> 1487
<212> DNA
<213> Homo sapiens

<400> 409
cggacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50
tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100
cagcatttaa tgaaaaatth atgcttaaga agtaaaaatg gcaggcttcc 150
tagataatth tcgttgcca gaatgtgaat gtattgactg gactgagaga 200
agaaatgctg tggcatctgt tgcgcaggt atattgtttt ttacaggctg 250
gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300
accatgcctt tcacacatgt ggtgtattht ccacattggc thtttcatg 350
ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400
ctgttttagga agaacagggtg ctcgagtttg gctthttcatt ggtthcatgt 450
tgatgttttg gtcacttatt gcttccatgt ggattcttht tggatcatat 500
gttaccctaaa atactgatgt ttatccggga ctagctgtgt thtttcaaaa 550

tgcacttata	tttttttagca	ctctgatcta	caaatttgga	agaaccgaag	600
agctatggac	ctgagatcac	ttcttaagtc	acattttcct	tttgttatat	650
tctgtttgta	gatagggtttt	ttatctctca	gtacacattg	ccaaatggag	700
tagattgtac	attaaatggt	ttgtttcttt	acatttttat	gttctgagtt	750
ttgaaatagt	tttatgaaat	ttctttattt	ttcattgcat	agactgttaa	800
tatgtatata	atacaagact	atatgaattg	gataatgagt	atcagttttt	850
tattcctgag	atttagaact	tgatctactc	cctgagccag	ggttacatca	900
tcttgtcatt	ttagaagtaa	ccactcttgt	ctctctggct	gggcacggtg	950
gctcatgcct	gtaatcccag	cactttggga	ggccgaggcg	ggccgattgc	1000
ttgaggtcaa	gtgtttgaga	ccagcctggc	caacatggcg	aaaccccatc	1050
tactaaaaat	acaaaaatta	gccaggcatg	gtggtgggtg	cctgtaatcc	1100
cagctacctg	ggaggctgag	gcaggagaat	cgcttgaacc	cggggggcag	1150
aggttgcagt	gagctgagtt	tgcgccactg	cactctagcc	tgggggagaa	1200
agtgaaactc	cctctcaaaa	aaaagaccac	tctcagtatc	tctgatttct	1250
gaagatgtac	aaaaaaatat	agcttcatat	atctggaatg	agcactgagc	1300
cataaaaggt	tttcagcaag	ttgtaactta	ttttggccta	aaaatgaggt	1350
tttttttggt	aagaaaaaat	atttgttctt	atgtattgaa	gaagtgtact	1400
tttatataat	gattttttta	atgcccaaag	gactagtttg	aaagcttctt	1450
ttaaaaagaa	ttcctcta	atgactttat	gtgagaa	1487	

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<210> 410
<211> 158
<212> PRT
<213> Homo sapiens
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<400>	410														
Met	Ala	Gly	Phe	Leu	Asp	Asn	Phe	Arg	Trp	Pro	Glu	Cys	Glu	Cys	
1				5					10					15	
Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala	
				20					25					30	
Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala	
				35					40					45	
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr	
				50					55					60	
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val	
				65					70					75	

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu
80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu
95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr
155

<210> 411

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 411

gtttgaggaa gctgggatac 20

<210> 412

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 412

ccaaactcga gcacctgttc 20

<210> 413

<211> 40

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-40

<223> Synthetic construct.

<400> 413

atggcaggct tcctagataa ttttcggttg ccagaatgtg 40

<210> 414

<210> 415
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 415
 Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
 1 5 10 15
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
 20 25 30
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
 35 40 45
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
 50 55 60
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
 65 70 75
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
 80 85 90
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
 95 100 105
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
 110 115 120
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
 125 130 135
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
 140 145 150
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
 155 160 165
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
 170 175 180
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
 185 190 195
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
 200 205 210
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
 215 220

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-21
 <223> Synthetic construct.

 <400> 416
 gccatagtca cgacatggat g 21

 <210> 417
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 417
 ggatggccag agctgctg 18

 <210> 418
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 418
 aaagtacaag tgtggcctca tcaagc 26

 <210> 419
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 419
 tctgactcct aagtcaggca ggag 24

 <210> 420
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 420
 attctctcca cagacagctg gttc 24

<210> 421
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 421
gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
cacgccagga gctogctcgc tctctctctc tctctctcac tctcctctcc 200
ctctctctct gctgtccta gtcctctagt cctcaaattc ccagtcccct 250
gcaccccttc ctgggacact atgttgttct ccgccctcct gctggaggtg 300
atgttgatcc tggctgcaga tgggggtcaa cactggacgt atgagggcc 350
acatggtcag gaccattggc cagcctctta cctgagtgt ggaaacaatg 400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
ggacctgcac aacaatggcc acacagtga actctctctg ccctctaccc 550
tgtatctggg tggacttccc cgaaaatatg tagctgccc gctccacctg 600
cactggggtc agaaaggatc ccagggggg tcagaacacc agatcaacag 650
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700
atgacagctt gagtgaggct gctgagaggc ctcaggcct ggctgtcctg 750
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900
cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950
gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000
ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggta 1050
cagaactacc gagcccttca gcctctcaat cagcgcatgg tctttgcttc 1100
tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150
gtgtaggaat cttggttggc tgtctctgcc ttctcctggc tgtttatttc 1200
attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt 1250
cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac 1300
catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg 1350
gggtgtagga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400
ccttccccctg gacatctctt agagaggaat ggaccaggc tgtcattcca 1450
ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500
gaaatcgctg tgttgttaat gcagaganca aactctgttt agttgcaggg 1550
gaagtttggg atatacccca aagtcctcta cccctcact tttatggccc 1600
tttccttaga tatactgcgg gatctctcct taggataaag agttgctgtt 1650
gaagttgtat atttttgatc aatatatttg gaaattaaag tttctgactt 1700
t 1701

<210> 423
<211> 337
<212> PRT
<213> Homo sapiens

<400> 423
Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala
1 5 10 15
Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln
20 25 30
Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
35 40 45
Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
50 55 60
Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
65 70 75
Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 424
gtaaagtcgc tggccagc 18

<210> 425
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 425
cccgatctgc ctgctgta 18

<210> 426
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 426
ctgcactgta tggccattat tgtg 24

<210> 427
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 427
cagaaacca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
aatttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50
acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100
gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

Thr Pro Gly Thr Gln Thr His Pro Leu Thr Leu Gly Gly Leu Asn
 80 85 90
 Val Gln Gln Gln Leu His Pro His Val Leu Pro Ile Phe Val Thr
 95 100 105
 Gln Leu Gly Ala Gln Gly Thr Ile Leu Ser Ser Glu Glu Leu Pro
 110 115 120
 Gln Ile Phe Thr Ser Leu Ile Ile His Ser Leu Phe Pro Gly Gly
 125 130 135
 Ile Leu Pro Thr Ser Gln Ala Gly Ala Asn Pro Asp Val Gln Asp
 140 145 150
 Gly Ser Leu Pro Ala Gly Gly Ala Gly Val Asn Pro Ala Thr Gln
 155 160 165
 Gly Thr Pro Ala Gly Arg Leu Pro Thr Pro Ser Gly Thr Asp Asp
 170 175 180
 Asp Phe Ala Val Thr Thr Pro Ala Gly Ile Gln Arg Ser Thr His
 185 190 195
 Ala Ile Glu Glu Ala Thr Thr Glu Ser Ala Asn Gly Ile Gln
 200 205

<210> 430

<211> 1257

<212> DNA

<213> Homo Sapien

<400> 430

ggagagagggc gcgcgggtga aaggcgcatt gatgcagcct gcggcggcct 50
 cggagcgcg cgagagccaga cgctgaccac gttcctctcc tcggtctcct 100
 ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
 gccccgccgc ctccccgcag cggtccgcg gctcctgct gctcctgctg 200
 ctgcagctgc ccgcgccgtc gagcgcctct gagatcccca aggggaagca 250
 aaaggcgag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
 gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
 aatgttatcc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
 agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacacca 450
 actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500
 aaaattgcgg agtgtacatt tacaagatg cgttcaaata gtgctctaag 550
 agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600
 agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650

attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700
aattaatatt catcgcaactt cttctgtgga aggactttgt gaaggaattg 750
gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900
ttattatgcc ttggaatggt tcaacttaaata gacattttta ataagtttat 950
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000
tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050
aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100
acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200
aatttgtaaa tgtaagaat tttttttata tctgttaaata aaaaattatt 1250
tccaaca 1257

<210> 431
<211> 243
<212> PRT
<213> Homo Sapien

<400> 431
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
1 5 10 15
Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
20 25 30
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
35 40 45
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
50 55 60
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	

Leu Pro Lys

<210> 432
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial Sequence

<400> 432
 aggacttgcc ctcaggaa 18

<210> 433
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 433
 cgcaggacag ttgtgaaaat a 21

<210> 434
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 434
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